

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANTS: Reed, Steven G.  
Skeiky, Yasir A.W.  
Dillon, Davin C.  
Campos-Neto, Antonio  
Houghton, Raymond  
Vedvick, Thomas S.  
Twardzik, Daniel R.  
Lodes, Michael J.  
Hendrickson, Ronald

(ii) TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY  
AND DIAGNOSIS OF TUBERCULOSIS

(iii) NUMBER OF SEQUENCES: 355

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SEED and BERRY LLP  
(B) STREET: 6300 Columbia Center, 701 Fifth Avenue  
(C) CITY: Seattle  
(D) STATE: Washington  
(E) COUNTRY: USA  
(F) ZIP: 98104-7092

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE: 05-MAY-1998  
(C) CLASSIFICATION:

(vii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Maki, David J.  
(B) REGISTRATION NUMBER: 31,392  
(C) REFERENCE/DOCKET NUMBER: 210121.411C9

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (206) 622-4900  
(B) TELEFAX: (206) 682-6031

## (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 766 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

10034311-2 22502

## (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGAGGCACCG	GTAGTTGAA	CCAAACCCAC	AATCGACCGG	CAAACGAAACG	GAAGAACACA	60
ACCATGAAGA	TGGTAAATC	GATGCCGCA	GGTCTGACCG	CCGCGGCTGC	AATCGGGGCC	120
GCTGGGGCG	GTGTGACTTC	GATCATGGCT	GGCGCCCGG	TGTTATACCA	GATGCAACCG	180
GTCGTCTCG	GGCGCCACT	GGCGTTGAC	CGGGCATCGC	CCCTTGACGT	CCCGACCGCC	240
GCCCAGTGA	CCAGCTCTGT	CAACAGCTC	ACGATGCCA	ACGTGTCGTT	TGCGAACAAQ	300
GCGAGCTCG	TCGAGGGGG	CATCGGGGC	ACCGAGGGCC	GCATCGCGA	CCACAACTG	360
AAGAAGGGCG	CGCAGCACCG	GGATCTGCC	CTGTCGTTCA	GCCTGACGAA	CATCCAGCCG	420
GGGGCGGCC	GTTGGCCAC	CGCGGACGTT	CTCGTCTCGG	GTCCGAAGCT	CTCGTCGCCG	480
GTCACCGAGA	ACGTCACCTG	CGTGAATCAA	GGCGCTGGA	TGCTGTCAGC	CGCATCGGG	540
ATGGAGTTGC	TGCAAGCCG	AGGGNAACT	ATGGCCGAC	GGGNTTCAGC	CCCGTGTTC	600
GCTACGCCCG	CGCGCTGGAT	ACGTCATCAT	GTGCAACACT	CGCGGTGTA	GCACGGTGCG	660
GTNTGGCGAG	GGNCGCACCG	ACCGCCCGGT	GCAAGCCGTC	CTCGAGAGATAG	GTGGTGNCTC	720
GNCACCAAGNG	ANCAACCCCN	NNTCGNCNNT	TCTCGNTGNT	GNATGA		766

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGCATCAC	ATCACCATCA	CGATGAAGTC	ACGGTAGAGA	CGACCTCGGT	CTTCCGCGCA	60
GACTTCTCA	GCGAGCTGGA	CGCTCCCTGCG	CAAGCGGTA	CGGAGAGGGC	GGTCTCCGGG	120
GTGGAAGGGC	TCCCAGCCGG	CTCGCGCTTG	CTGGTAGTCA	AACGAGGGCC	CAACGCGGGG	180
TCCCGGTTCC	TACTCGACCA	AGGCATCACG	TCGGCTGGT	GGCATCCCGA	CAGCGACATA	240
TTTCTCGAGC	ACGTCACCGT	GAGCGCTCGG	CATGCTGANT	TCCGTTGGA	AAACAAACGAA	300
TTCAATGTG	TGATGTCGG	GAGTCTCAAC	GGCACCTAGG	TCAACCGGA	GCCCGTGGAT	360
TCGGCGGTG	TGGCGAACCG	CGACGAGGTC	CAGATGGCA	AGCTCCGGTT	GGTGTCTT	420
ACCGGACCCA	AGCAAGGGCA	GGATGACGGG	AGTACCGGGG	GCCCCGTGAGC	GCACCCGATA	480
GCCCCCGCT	GGCCCGGGATG	TCGATCGGG	CGCTCTCTGG	ACCTGCTACG	ACCGGATTGTT	540
CCCTGATGTC	CACCATCTCC	AAGATTCGAT	CTTGGGAGG	CTTGAGGGTC	NGGGTACCC	600
CCCCGGGGC	CTCATTCNGG	GGTTTCGCGN	GGTTTCACCC	CNTACCNACT	GCNCNNCGGN	660
TTGCAATT	NTTCTTCNCT	GCCCNNAAG	GGACCNNTTAN	CTTCCGCTN	GAANGGTNA	720
TCCNGGGCCC	NTCTCTGAA	CCCCNTCCCC	CT			752

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATATGCATC	ACCACATACCA	TCACACTTCT	AACCGCCCG	CGCGTCGGGG	GCGTCGAGCA	60
CCACCGCACA	CGGGGCCG	TCGATCTGCT	AGCTTGAGTC	GGTTCAGGCA	TCGTCGTCAG	120
CAGCGCGATG	CCCTATGTT	GTGTCGACT	CAGATATCGC	GGCAATCCAA	TCTCCCGCCT	180

GC GGCC CGCG	GT GCT GCAA	CT ACT CCCG	AG GAATT TCG	AC GTG CGC AT	CA AGA TCT TC	240
AT GCT GGT CA	CG GCT GTC GT	TT GCT CTG T	TG TCG GTG	TG GCG AC GG	CG GCG CC AA	300
AC CT ACT CG	AG GAG TT GAA	AG GCA CG AT	AC CG GCG C	AG TGC CAG AT	TC AA A TG TCC	360
GAC CGG CCT	AC A AC AT CA	CAT CAG CCT G	CC CAG TTA CT	AC CCG GAC CA	GA AG TCG CTG	420
GAA AA TT A CA	TC GCG CC AG AC	GC GCG AC A AG	TT CCG TCA CG	CG GCG CA CAT C	GT CCA CT CCA	480
CG CGA AG C CC	CCT AC GA ATT	GA AT AT CAC C	T CG GCG CA CT	AC CAG TCG C	GAT ACC CG CG	540
CG TGT GTC AG	AG GCG GT TGG	GCT CAG MG TC	TAC CAC A CA	CG GCG CC AC	GC ACC CA AC	600
AC CA CG TAC A	AG GCG CT TCG A	TT GGG CAG AC	GC CT AT CG CA	AG GCA AT CA C	CT AT GAC AC	660
CT GT GCG AG	CT GAC AT CG	TC GCG CT CCA	GT GCT CT TCC	CC AT TGT TGC	AAG GTG AACT	720
GAG CA ACC CA	GA CG GGA CA	AC WGG TAT CG	AT AGC GGC CN	AAT GCG GCT	TG GAA ACC CNG	780
TG AAA ATT AT C	ACA ACT TCG C	AG TCA CNA A A	NAA			813

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CG GT AT GAA C	AC GG CC CG CG	CC GATA AACT T	CC AG CT GT TCC	CAG GGT GGG C	AG GG AT TC CG	60
CAT TCC GAT C	GG GCG AG CG A	TGG GAT CG C	GG GCG AG AT C	CG AT CG GGT G	GG GGG T CACC	120
CAC CG TT CAT	AT CG GGG C CT A	CC CG CTT CCT T	CG GCG TT GGG T	GT GTC GAC A	AC A AC CG CA	180
CG GCG AC AG CG A	GT CCA AG CG C	TG GTC CG GAG	CG CT CG CG G	GC AA GT CT CG	GC AT CT CC AC	240
CG CG AC CG CT G	AT CA CG CG CG	TC GAC CG CG C	TCC GAT CA AC	TC GCG CA CC G	CG AT GCG GGA	300
CG CG CT TA C	GG GCA TAT C AT C	CC CG GT GAC GT	CAT CT CG GT G	AA CT GG CAA A	CC AAG TCG GG	360
CG GCA CG CG T	AC A CG G A AC G	TG AC AT TG GC	CG AG GG ACC C	CC CG CC TG AT	TT CG TCG Y GG	420
AT ACC ACC CG	CC GG CG CG CC	AAT TGG G				447

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GT CCC ACT GC	GG TCG CG GAG	TAT GT CG C CC	AG CAA AT GTC	TGG CAG CGC G	CC AAC GGA AT	60
CG CG GT AT CC	GAC GTC CG AG	GT TGT CG A AC	CG CG CG CG C	GG AAG TAT CG	GT CCA TG CCT	120
AG CCC CG CG A	CG CG CA G CG C	CG GAA AT TG CG	CG AG TGA GGA	GG CG CG CA AT	TT GG CG GGG C	180
CG CG CG AC CG G	NG AG CG CG CG	AAT CG CG CG A	GT GAG GAG GT	GG NC AG TCA T	GC CC AG NG NT G	240
AT CC AA TCA A	CCT GN AT TCG	GN CT GN GGG N	CC AT TT GAC A	AT CG AG GT AG	TG AG CG CAA A	300
TGA AT GAT CG	AAA AC CG GG G	GN GAC GT CG C	NT GT GT CT GGT	GG TGT NAG GT	GN CT GN CT GG	360
NG TGN NG NG NT	AT CAG AT GAT GT	TCT CG NC G	AA NT CT GAT GN	CG AG GAA CG AC	GG GT GN TCC GG	420
NN AN NN CC NN	GG NG NG CN AN	CC CN NN NN TCC	TC GNG CNA AT	CAN AN AG NC G	NT TG AT GN GA	480
AAA AAG GT G	GANC AGN NNN	AA NT NG NG GN	CC NA AN A NC	NN NN AN NG NN	NN AG NT NG NT	540
NN NT TT NN NC	AN NN NN NN NT	NN NG NG NN CN	NN NC AN CN	NN NG NG NN NA	NN NG NG NT NN	600
NN AT						604

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTGCANGTCG	AACCACCTCA	CTAAAGGAA	CAAAGCTNG	AGCTCCACCG	CGGTGGCGGC	60
CGCTCTAGAA	CTAGTGTGATM	YYCYKGGCTG	CAGSAATYCG	GYACGAGCAT	TAGGACAGTC	120
TAACGGTCTCT	TTTACCGTGA	TGCAATGACG	GACGACATTC	TGCTGATCGA	CACCGACGAA	180
CGGGTGGCAA	CCTCTACCCCT	CAACCGGGCG	CAGTCCTCGYA	ACGGGCTCTC	GGCGGCGCTA	240
CGGGATCGGT	TTTTCGCGGY	GTTGGYCGAC	GCCGAGGYYCG	ACGACGACAT	CGACGTCGTC	300
ATCCCTCACCG	GYGCCCGCTC	GTTGTTCTGC	GGCGGACTTC	ACCTCAAGGT	AGCTGGCCGG	360
CGACAGCCCG	CTGGCGGACA	TCTACCCGGC	GTGGCGGCG	ATGACCAAGC	CGTGATCGAC	420
CGCGATCAAC	GGCGCCGGG	TCACCGGGG	GCTCGAACTG	GCGCTGTACT	GCGACATCTC	480
GATCGCTCC	GACGACGCC	GCTTCGNGGA	CACCCACGCC	CGGGTGGGGC	TGCTGCCCCAC	540
CTGGGGACTAC	AGTGTGTGT	TGCGCAAAA	GGTCGGCATC	GGNCTGGGCC	GGTGGATGAG	600
CCTGACCCGC	GACTACCTGT	CGGTGACCGA	CGC			633

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGACGACGAC	GGCGCCGGAG	AGCGGGCGCG	AAACGGCGATC	GACGCGGCC	TGGCCAGAGT	60
CGGCACCCCG	CAGGAGACACT	TGCAATCATG	AAATTATGCA	ACCATATTGA	GCCCGTGCAG	120
CCCCCGCGAG	CCGGGGGGCG	GGTCCCGCCG	GTCCTATGCC	AGGCCCCCGC	CGAGTTCGGC	180
CGGCTGCGG	AGCCGCTCGC	CATCTGTCC	CCGGACGAGG	GACTGCTCAC	CGCCGGCTGG	240
GCGACGTGTC	CGCAGAGACT	GCTGGTGGGC	CAGGTGGCGC	GTGGCGGCAAA	GGAAAGCCGTC	300
GGCCGGCGG	TGCGGGCCAG	CCTCGCTGCG	CCCTGGTGGC	TGACGACACA	CACCACCATG	360
CTGTACGGGG	CAGGCCAAC	CGAACACGCC	GGGGCAGATCT	TGGCCGGAC	AGCACCTGCC	420
GCCGGTGACC	GAACAGGCC	GTATGTGGG	TGGGGCGGAC	GAACCCGGGAC	ACCGGGGGGA	480
CCGGGGCGAC	CGTGGCGGCC	GGATGTGCCG	GGCGAACATTAC	TGGGCACCGC	GTGCAATTTC	540
CACTTCATCG	CACGCCCTGGT	CCTGGTCTCG	CTGGACGAAA	CCTTCCTGCC	GGGGGGCCCG	600
CGGCCCGAAC	AGCTCATCGG	CGCGGCCCGT	GGACTGGTGT	TGGCCCGGCA	GGTGGCGCGG	660
GAGCATCGGC	CGGGCGCTCG	CACCCCGCCG	CTCGAGCGCG	GAACGCTGCC	CGACGATCTG	720
GCATGGCAA	CACCGTCCGA	GCCCCATAGCA	ACCGCGTTCG	CCCGCGCTCAG	CGACCACCTG	780
GACACCGGCC	CGCACCTGCC	GCCACCGACT	CGTCAGGTGG	TCAAGGGGGGT	CGTGGGGTCC	840
TGGCACGGCG	AGGCAATGCC	GATGAGCAAGT	CGCTGGACGA	ACGAGCACAC	CGCCGAGCTG	900
CCCGCCGACCC	TGCAACGCGCC	CACCCGTCTT	GGCCCTGCTG	CCGGCCCTGGC	CCCGCATCAG	960
GTGACCGACG	ACGACGTCGCG	CGCGGCCCGA	TCCCTGCTCC	ACACCGATTC	GGCGCTGGTT	1020
GGCGCCCTGG	CCTGGGGCCG	CTTACCCGCC	GGCGGGCGCA	TCGGCACCTG	GATCGGGGCC	1080
GGCGCCGAGG	GCCAGGTGTC	CGCGCAAAAC	CCGACTGGGT	GAGTGTGCGC	GCCCCTGTGCG	1140
TAGGGTGTCA	TGCTCTGGCC	GAGGGATCTC	GGCGGGCGCA	ACGGAGGTGG	CGACACAGGT	1200
GGAAAGCTGGC	CCCATCTGGCT	TGCGCCCCAA	CGCCGCTGTG	GGCGTTGGGT	TGCGCCCACT	1260
GGCGGATCAG	GTCCGGCGCC	GCCCTTGGCC	GAAGGTCCAG	CTAACGTC	CGTCACCGAA	1320
GGACCGGACG	GTCACCGGGG	GTCACCCCTGC	CGGCCCAAGG	AA		1362

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCAGACGACCC	CGATATGCCG	GGCACCGTAG	CGAAAGCCG	CGCCGACGCA	CTCGGGCGCG	60
GTATCGCTCC	CGTGTGAGAC	ATCTCAGGG	CGCTGGAGGC	CGGGCTGGGG	GAAGCCGGTC	120
TGGATGACGT	GGCCGCTGTT	TACATCATCT	ACCGGCAGCG	CGCCGCCAGAG	CTGCGGACGG	180
CTAAGGCCCT	GCTCGGGCTG	CGGGGACGAGT	TAAGCTGAG	CTTGGCGGCC	GTGAGGGTAC	240
TGCGCGAGCG	CTATCTCGCT	CAGACGAGGC	AGGGCCGGG	GGCCGAGTCG	ACCGGGCAGAC	300
TGATGGACCC	ATCGGCGCG	TGTGTCGCGG	CGGGGAGGAG	CCAGTATGAG	CGGGGCTCGT	360
CGAGGGCGTG	GGCCGAGCGG	TTCGCACCGC	TATTACGCAA	CCTGGAATTTC	CTGCGGAATT	420
CGGCCAGCTT	GATGAACCT	GGCACCGAGC	TGGGACTGCT	CGCCGCGTGT	TTTGTCTGCG	480
CGATGGAGGA	TGATCTGCAA	TGATCTTGTG	CGACGCTGGG	ACAGGCCGCC	GAGCTGCAGC	540
GGGCTGGAGG	CGGCACCGGA	TATGCGTCA	GCCACCTGGG	ACCCGCCGGG	GATCGGGTGG	600
CCTCCACGGG	CGGGCACGGC	AGGGCACGGG	TGTCGTTCTT	ACGGCTGTAT	GACAGTGGCG	660
CGGGTGTGGT	ATCGATGGGG	GGTCGCGGG	TGTCGGGCTG	TATGGCTGTG	CTTGATGTGT	720
CGCACCGGA	TATCTGTGAT	TTCTGTACCC	CCAAGGGCGA	ATCCCCCAGC	GAGCTCCCGC	780
ATTCACCACT	ATCGGTGTTG	GTGACCGACG	TGCTCTCGG	GGCCGTCGAA	CGCAACCGCC	840
TACACGGGG	GGTCAATTCG	CGAACCGGA	AGATCGTCG	CGGGATGCC	GCGGCCGAGC	900
TGTTGACGGC	CATCTGCAAA	GGCCGCACAC	CCGGTGCGGA	TCCCAGGCTG	GTGTTCTCG	960
ACACGATCAA	TAGGGAAAC	CCGGTGGCGG	ATGGGCTGAT	ACCGAGGGG	ACCAACCCGT	1020
CGGGGGAGGT	CCCACTGCTG	CCTTACGAGT	CATGTAATCT	CGGGCTGATC	AACCTGCC	1080
GGATGCTGCG	CGAGGGTCGC	GTGCACTGGG	ACGGGCTCGA	GGAGGTCGCC	GGTGTGGGG	1140
TGCGGTTCTT	GTATGACGTC	ATCGATGTC	GGCCGCTACCC	CTTCCCCGAA	CTGGGTGAGG	1200
CGGGCCGGGC	CACCCGCAAG	ATCGGGCTGG	GAGTCATGGG	TTTGGCGGAA	CTGCTTGC	1260
CACTGGGTAT	TCCGTACGAC	AGTGAAGAAG	CCGGTGGCTT	AGCCACCGG	CTCATGCGTC	1320
GCATACAGCA	GGCGGCCAC	ACGGCATCGC	GGAGGCTGGC	CGAAGAGGGG	GGGCCATTC	1380
CGGGGTTAAC	CGATAGCGGC	TTCCGCGGGT	CGGGGCCAGG	GGCAACGCA	CAGGTCACT	1440
CCGTCGCTCC	GACGGGA					1458

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 862 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGGTGTAAT	CGTGTGGAT	CTGGAACCCG	GTGGCCCGT	ACCTACCGAG	ATCTACTGGC	60
GGCCGAGGGG	GCTGGCCCTG	GGCATCCCGG	TGTCGCTAGT	CGGGATCGGG	GTGGCCCATCG	120
TCATGCCCTT	CGTGTGACAGC	AGGCCCGTGT	CCAAACCGGT	CAGCGCCQAC	AAGCCGGCT	180
CCGCCAGAG	CCATCCGGGC	TGCGCCGAC	CCAAAGCACCC	CGAGCCGGG	GGGCAAACCG	240
AAGGTAACCG	GGCCGCGGCC	CCGCCGAGGG	GGAAAACCC	CGAGACACCC	ACGCCAACCG	300
CCGGGTGCGA	GGCCGCGGCC	GTGCTCAAGG	AAAGGGACGA	TGGCCCCGAT	TCGAGGCTGG	360
CCGTCAAAGG	TTTGACCAAC	CGGCCGAGGT	ACTACGTCGG	CGACCGAGGG	AGTTACCCA	420
TGGGTGCGCA	CAACATCGGC	TGCTGTCTT	GTAAAGCGGA	CGTTGGGGCC	CGGGTGTGTTG	480
CCGGCTAGGT	TTACTCTGCTG	GACACAAACG	GGTTGTGTC	CAACCTGGAC	TGCGGGCCCT	540
CGAATGAGAC	GCTGGTCAG	ACGTTTCCC	CCGGTGAGCA	GGTAACGACC	CGGGTGACCT	600

GGACCGGGAT	GGGATCGCGC	CCGCGCTGCC	CATTGCCGCG	GCCGGCGATC	GGGCCGGGCA	660
CCTACAATCT	CGTGTACAA	TCTGGCAATC	TGCGCTCGCT	GCCGGTTCGG	TTCATCTTGA	720
ATCAGCCGCC	GCCGCCGGCC	GGGCCGGTAC	CCGGCTCGGG	TCCAGCGCAG	GCCGCTCCGC	780
CGGAGTCTCC	CGCGCAAGGC	GGATAATTAT	TGATCGCTGA	TGGTCGATTG	CGCCAGCTGT	840
GACAACCCCT	CGCCCTCGTGC	CG				862

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTGATCAGCA	CCGGCAAGGC	GTCACATGCC	TCCCTGGGTG	TGCAGGTGAC	CAATGACAAA	60
GACACCCCGG	GCGCCAAGAT	CGTCGAAGTG	GTGGCCGGTG	GTGCTGCCG	GAACGCTGG	120
GTGCCGAAGG	GGCTGCTTGT	CACCAAGGTC	GACGACGCC	CGATCACAG	CGGGAGCGG	180
TTGGTGGCCG	CGCTCGGTC	AAAGCGCCG	GGGCCCAAGG	TGGGGCTAAC	CTTTCAAGGAT	240
CCCTCGGGCG	GTAGCGGCC	AGTGAAGCT	ACCTCTGGCA	AGGGAGAGCA	GTGATGAAGG	300
TCGCCGCCGA	GTGTTCAAG	CTCGGATATA	CGTGGCACC	CATGGAACAG	CGTGGCAGGT	360
TGGTGTGTTG	CGGGCGACTT	GTGCTGTCG	TTGACGATCG	ACGGCGCAC	GGGGATGAAG	420
ACCAACAGCG	CGCTCTTGT	ACCGAGCTGC	TCACCGAGGG	CGGGTTGTT	GTGAGCGGCC	480
TGGTGGCGGT	GTCCGGCCGA	GAGGGTGAAGA	TCCGAAATGC	GTCTAACAC	GGGGTATCG	540
GGGGGGTTGA	CCTGGTGTG	TGGTCTGGGG	GGACCGGNGT	GACGNTCTGC	GATGTCACCC	600
CGGAAGCCAC	CCGNGACATT	CT				622

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCGCAGCGG	TAAGCTCTGT	GGCCGCCGGC	ACACTGGTGT	TGACAGCATG	CGGGGGTGGC	60
ACCAACAGCT	CGTCGTCAAG	CGCAGGGGA	ACGTCCTGGGT	CGGTGCACTG	CGGGGGCAAG	120
AAGGAGCTCC	CGCTCGGCG	CTCGACCGCA	AAAGAAATC	CCATGGAGCA	GTTCGCTCTAT	180
GCTCTAGCTC	GATCGTGGCC	GGGGCTACAGC	TTGGACTACCA	ACGGCAACGG	GTCCGGTGGCC	240
GGGGTGACCC	AGTTTCTCAA	CAACGAAACC	GATTTCGGCG	GCTCGGATGT	CCCGTTGAAT	300
CGGTCGACCG	GTCAACCTGA	CCGGTGGGG	GGGGGGTGG	GTTCGGGGGG	ATGGGACCTG	360
CGGACGGTGT	TGGGGCGAT	CGCGATCAC	TACAAATATCA	AGGGCGTGTG	CACGCTGAAT	420
CTTGACGGAC	CCACTACCGC	CAAGATTTC	AACGGCACCA	TCACCGTGTG	GAATGATCCA	480
CAGATCAAG	CCCTCAACTC	CGGCACCGAC	CTGGCGCCAA	CACCGATTAG	CGTTTATCTTC	540
CGCAGGGACA	AGTCCCGTAC	GTGCGACACA	TTCCGAAAT	ACCTCGAGGG	TGTTATCCAAC	600
GGGGCGTGGG	GCAAAGGGCG	CRCGCAAACG	TTCACTGGGG	GGCTCGGGGT	CGGCGCAGC	660
GGGAACACAGC	GAACGCTGCC	TCTACTCGAC	ACGACCGAGC	GGTGTGATCAC	CTACAAACAG	720
TGGTCCTTTC	CGGGGGTAA	CGACTGTGAA	ATGGGCGCAA	TCATCACGTC	GGGGGGTCCG	780
GATCCAGTGG	CGATCACAC	CGAGTCGGTC	GGTAAAGACAA	TGCGGGGGC	CAAGATCATG	840
GGACAAAGCGA	ACGACTCTGT	ATGGGACAGC	TGGCTGTCT	ACAGACCCAC	CCAGCCCTGGC	900
TCTTACCCCGA	TGGTGTGGCG	GACCTATGAG	ATCGCTGTCT	CGAAATACCC	GGATGCGACG	960
ACCGGTACTG	CGGTAAGGGC	GTTTATGCAA	GCCGCGATTG	GTCCAGGCCA	AGAAGGCCCTG	1020

GACCAATACG GCTCCATTCC GTTGCCAAA TCGTTCCAAG CAAAATTGGC GGCGCGGTG  
 AATGCTATT CTTGACCTAG TGAAAGGGAT TCGACGTTGA GCGATGCCGT TCCGACAGTA  
 GGGTCGCAAT TTGGGCCGTA TCAGCTATTG CGGCTGCTGG GCCGAGGCAG GATGGGCAG  
 1080  
 1140  
 1200

## (2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1155 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCAAGCAGCT GCAGGTCGTC CTGTTGACG AACTGGCAT GCGGAAGAAC AAACGCACCA	60
AGACCGGCTA CACCAACGGAT GCGGACCGC TGCACTGCTT GTTCGACAAAG ACCGGGCATC	120
CGTTTCTGCA ACATCTGCTC GCCCACCGCG ACCTCAGCCCG GTCTCAAGGTC ACCGTCGACG	180
GGTTGCGCA ACAGGGTGGCC GCGCACCGCC GCACTCACCAAC CAGCTTCACAC CAGACGATCG	240
CCGGCACCGG CGCGCTCTCC TCAGACGGAAC CCAACCTGCA GAACATCCCG ATCCGACCCG	300
ACGGCGGGCGG CGGGATCCGG GACCGCTTCG TGTTGCGGGG CGGTTACGGCC GAGTTGATGA	360
CGGGCGGACTA CAGCGGACGAGATGCGCA TCATGGGGCA CCTGTCGGGG GACGAGGGCC	420
TCATCGAGGC GTTCAACACC GGGGAGGAGC TGTTATTGTT CGTGCCTGCG CGGGTGTTCG	480
GTGTCGGCCAT CGACGGAGTC ACCGGCGAGT TGCGGCGCCCG GTGCAAGGGC ATGTCCTACG	540
GGCTGGCTTC CGGGTGTGAGC GCCTACCGCC TGTGCGGACAA GTTGAATAATC TCCACCGAGG	600
AAGGCAACGA CGACATGGAC GCGTATTTCG CCGGATTCGG CGGGGTGCGC GACTACCTGC	660
GCGCGCTAGT CGAGGGGGCC CGCAAGGAGC GCTACACCTC GACGGTCTCG GGCGCTCGCC	720
GCTACCTGCC CGAGGCTGGC AGCACGACCG GTCAGTGGCG GGAGGCCGCC GAGCGGGCGG	780
CGCTGAACGC GCGATTCAGG GGCAGCGGCC CGGACATCAT CAAGGTGGCC ATGATCCAGG	840
TGCGAACAGC GCTCAACAGG GCACATGGCA CGTGCCTCGA GTGTCGTCGA GTCCACGAGC	900
AGCTGCTGTT CGAACATGCC CCCGGTGAAC CGCAGCGGGT CGAGGCCCTG GTGCGCGACA	960
AGATGGCGCG CGCTTACCCG CTGACGCTC CGCTGGAGGT GTCGGGGGCC TACGGCCGCA	1020
GCTGGGACGC GGCGGACGAC TGAGTGGCGA GCGTGCATCT GGGGGGGGAA TTGGGGGATT	1080
TTTCCGGCTT AGATTCAACG TCGGGCCAAT CGGGACCGAG TTGTCGACG GTGTACCCGT	1140
CGAGTAGCTT CGTCA	1155

## (2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1771 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCGCCGTC TGGTGTTCGA ACGGTTTAC CGGTGCGCAT CGGCACGGGC GTTGCGGGGT	60
TCGGGCTTCG GGTGTCGCGAT CGTCAACAG CGTGGTGCCTCA ACCACGGGGC ATTGCTGGC	120
ATCGAAAGACA CGCACCCAGG CGGGCACGCC CTTGAAAGCT CGATTTCAGT GCTGCTCCCC	180
GGCGCTGGGA TGCGGATTCC CGACGTTCCC GGTGCGACGG CTGGCGCTCG GAGCACCGAC	240
ATCGGAGAAGT CTGGGGGTTG GCGGACAGTT ATCTCAGTG ATCTCAGTC CACGCGGCCA	300
ACCTAGTTGT CGAAGTACTG TTGAAAGCCA CACCATCGA AGTCACCGCA TGGCCAAGTT	360
GGCCCGAGTA GTGGGCTTAG TACAGGAAGA GCAACCTAGC GACATGACGA ATCACCCACG	420
GTATTCGCCA AGCCGGACG AGCCGGAAAC CCCAGGTTAT GCTCAGGGGC AGCAGCAAC	480
GTACAGCGAG CAGTTGCACT GGCGTTAACCC ACCGTCGGCC CGGCCCGACG CAACCCAGTA	540
CCGTCACACC TACGAGGCCT TGGGGTGTAC CGGGCGGGGT CTGATACCTG CGGTGATTCC	600

GACCATGACG	CCCCCTCTG	GGATGGTCG	CCAACGCC	CGTGCAGGC	TGTTGGCCAT	660
CGGGCGGTG	ACGATAGCGG	TGGTGTCCG	CGGCATCGC	GGCGCGGCC	CATCCCTGGT	720
CGGGCTAAC	CGGGCACCGG	CGGGCCCG	CGGGGGCCCA	GTGGCTGCCA	GGCGCGGCC	780
AAGCATCCCC	GCAGCAAAAC	TGCCCCCGG	GTCGTCGAA	CAGGTGGCGG	CCAAGGTGGT	840
GCCCCAGTGC	GTCATTTGG	AAACCGATCT	GGGCGCCAG	TCGGAGGAGG	GCTCCGGCAT	900
CATTCTGTCT	GGCGAGGGGC	TGATCTTG	CAACAACCC	GTGATCGCCG	GGCGCGCCAA	960
GCCTCCCTG	GGCAGTCGC	CGCCGAAAAC	GACGTAAC	TTCTCTGACG	GGCGGACCGC	1020
ACCCCTTACG	GTGGTGGGGG	CTGACCCAC	CAGTGTATC	GCGCTCGTCC	GTGTTCAAGG	1080
CGTCTCGGG	CTTCACCCGA	TCTCTCGG	TTCTCTCC	GACCTGAGGG	TCGGTCAGCC	1140
GGTGTCTGGC	ATCGGGTTCG	CGCTCGGTT	GGAGGGCGA	GTGACCAACGG	GGATGTCAG	1200
CGCTCTCAAC	CGTCAGATGT	CGACGACCGG	CGAGGCAGGC	AACCAGAACAA	CCGTGCTGGA	1260
CGCCATTCAAC	CGATCAACCC	CGGTAACTCC	GGGGGCGGCC	TGGTGAACAT	1320	
GAACGCTCAA	CTCGTGGAG	TAACCTCGC	CATTGCAACG	CTGGGGCGGG	ACTCAGCCGA	1380
TGCGCAGAGC	GGCTCGATCG	GTCTCGGTT	TGCGATTCCA	GTGCGACCGG	CCAAGCGCAT	1440
CGCCGAGCG	TTGATCAGCA	CGCCGAAAGC	GTACATGCC	TCTCTGGGTG	TGCAAGTGG	1500
CAATGACAAA	GACACCCCGG	GGCGCAAGA	GTGCGAAGTA	GTGCGCGGTG	GTGCTGCCG	1560
GAACGCTGGA	GTGCGCAAGG	GGCTCGTGTG	CACCAAGGTC	GACGACCGCC	CGATCACAG	1620
CGCGGAGCGC	TTGGTGGCCG	CGCTCGGTC	AAACCGCCG	GGGGGCCACGG	TGGCCTAAC	1680
CTTTCAGGAT	CCCTCCGGG	GTAGCGGCAC	AGTGCAGTC	ACCCCTGGCA	AGCGGGAGCA	1740
GTGATGAGG	TCGCGCGCA	GTGTTCAAGA	C			1771

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTCCACCGG	GTGGCGGCCG	CTCTAGAACT	AGTGGATCCG	CCGGGCTGCA	GGAAATTCGGC	60
ACGAGGATCC	GACGTGGAG	GTGGTGCAG	CCGGCGCCG	GGAAATGATCG	GTCCATGCC	120
AGCCCCCGA	CGGGGAGGCC	CGGAATGGCG	CGAGTGGAGG	GGGGGGCAAT	TTGGGGGGC	180
CCGGCGACGG	CGAGGGCGCC	AATGGGCGA	GTGAGGAGGC	GGGGCGATCTG	GGCCACGGT	240
ATCCAATCAA	CTCTGCTTCG	GCTGCGGGC	CCATTGACAA	ATCGAGGTAG	TGAGCGCAA	300
TGAATGATG	AAAACCGGGC	TTGACCTCG	CTGTGCTGTG	GGTGTCTAGGT	GGCTGCTGTG	360
CTTGTGGCT	ATCAGGATGT	TCTTCGGCGA	AACTCTGATCG	CGAGGAACAG	GGTGTCTCCG	420
TGAGCCGAC	GGCGCTGGAC	CCCCCGCTCC	TCGGCGAGAT	CAGGCACTCG	CTTGATGCGA	480
CAAAGGGTT	GACCAACGGT	CACGTAGCGG	TCCGAAACAC	CGGGAAAGTC	GACAGCTTGC	540
TGGGTATTAC	CACTGGCGAT	GTGCAAGCTC	GGGGCAATCC	GCTGCGGCCA	AAAGGGGTAT	600
GCACCTACAA	CGACGAGCG	GGTGGTCCG	TTCGGGTACA	AGGGCAACAC	ATTCGCGTGA	660
AACTGTTGCA	CGACTGGAGC	AACTCTGGGT	CGATTTCTGA	ACTGTCAACT	TCACCGTGC	720
TCGATCTTGC	CGCTGGGGTC	ACGGCACTCG	TGTCGGGTGT	CAGGAACCTC	CAAGGGCAAG	780
GTACCGGAATG	GATAGAGGA	ATTTCGACCA	CCAAAATCAC	CGGGACCATC	CCCGGAGGT	840
CTGTCAAGAT	GCTTGATCCT	GGCGCAAGA	GTGCAAGGCC	GGGACCGTG	TGGATTGCC	900
AGGACGGGCTC	GCACCGACTC	GTCCGAGCGA	GCATCGACTT	CGGATCCGG	TGATTCAAC	960
TCACGAGTC	GAATGGAAC	GAACCGGTCA	ACGTGCAATA	GGCGGAAGTT	GGCTCGACGC	1020
GTTGNTGAA	ACGCCCTTGT	GAACGGTGTG	AACGGNAC			1058

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTCTGGCA	CGAGAGGTGA	TCGACATCAT	CGGGACCAGC	CCACATCGT	GGGAACAGGC	60
GGCGCGGAG	CGCGTCAGC	GGGCAGGGGA	TAGCGTGTAT	GACATCGGG	TGCGCTCGGGT	120
CATTGACAG	GACATGGCG	TGGACAGGGC	CGGCAAGATC	ACCTACCGA	TCAAGCTCGA	180
AGTGTCTTC	AAGATGAGGC	CGGGCAGACC	CGCCTAGCAC	GGGCGGGCGA	GCAAGACGCA	240
AAATCGACCA	TTTTGGGTT	GATTGTGCG	ATTTTGTGTC	TGCTCGCCGA	GGCCTACCAAG	300
GGCGAGGCCA	GGTGTGGCTG	CTGCGGTATC	CAGGGCTGCA	TGCGGATTCC	GGCGGCCACCG	360
CCGGAGTTAA	TGCTTCGCGT	CGACGGGAAAC	TGGCGATTC	GCGGGNGAGC	TGATCGATGA	420
CCGTGGCCAG	CCCGTGTGATG	CCGGAGTTGC	CCGAGGAAC	GTGCTGCCAG	GGCGGTAGGA	480
AGCGTCTGGT	GGCGGGGGTG	CTGACGGGCT	CTGCTGCGC	CCTCAGTGGC	GCCAGCGAGC	540
GG						542

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 913 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCGGTGGCCGC	CGCGCCTCCG	TTGGCCCAT	TGCGCCGTC	GCCGATCAGC	TGCGCATCGC	60
CACCATCACC	GCCTTTCGG	CGCGCAGCGC	CGGTGGGCC	GGGGCGCCCG	ATGCCACCGC	120
TTGCGCTTGC	CGCGGCGCG	CGCCATTGTC	TAACAGCAC	CCGGCGGGGG	CACCGTTAAC	180
GCCGTCGCCA	CGCTCCGCG	CGCTGCCGT	TCAGGGCGG	GAAGCGGAAT	GAACCGCGCG	240
CAAGCCGCC	GCAGGACCCG	TGCGGCCGT	TCAGGGCCGC	CCGGCGGGGG	CGGCCAATTG	300
CCGAACAGCG	AMGACCGGTT	CGCCGACCG	CGCGCCGCGT	TAACGGCGGT	GCGGGGCGCC	360
GCCGCGGAG	CGGCCATTAC	CGCCGTTTAC	GGTGGTGTG	CCGGCTTAC	CGGGCGCGGC	420
GTTTGGCCCG	AAATTCGGG	GGGCGACCGC	AGACCCCGCG	GGGCCACCAT	TGCCCGCGG	480
CACCGAAACA	ACAGCCAAAC	GGTGGCCCG	GGCCCGCCGT	TTGGCGCCAT	CACCGGCCAT	540
TCACCGCCAG	CACCGGGTT	ATTTGTTATG	AACCGGTAC	CGCCAGCGG	GCCCTTATTG	600
CGGGCGCCCG	GAAGNGGTGC	CGGGCGCCG	CGCCAAGGCC	AAAAAGCCCG	GGGTGCGCAC	660
CGGGCCCGG	GAACCCACCG	GTCCCCCGGA	TCCCCCGGT	GGCGCGCGT	CGCGCGCCAT	720
TGGTGTGCT	GAAGCCGCTC	CGGGCGGTT	CGCGGGTGTG	GGGGTGGGG	CTNTGGCCG	780
CGGGCCCGCC	GTTCGGTAC	AGCCACCCCC	CGGTGGGCC	GTGCGGCCA	TTGCGGCCAT	840
TGCGCCGGTT	CGCCGCTATG	CGCGCGTTC	CGCCGCAC	GCGGGNTTGG	CGCGCGGCCG	913

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1872 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACTACGTTG	GTGTAGAAAA	ATCCTGCCGC	CGGGACCCCTT	AAGGCTGGGA	CAATTCTGA	60
TAGCTACCCC	GACACAGGAG	GTTACGGGT	GAGCAATTG	CGCGGCCGCT	CACTCAGGTG	120

GTCATGGTTG	CTGAGCGTGC	TGGCTGCCGT	CGGGCTGGGC	CTGGCCACGG	CGCCGCCCGA	180
GGCGGCCCG	CCGGCTTGT	CGCAGGACCG	GTTCGCGAC	TTCCCGCGC	TGCCCCCTCGA	240
CCCGTCGCG	ATGGTCGCC	AAAGTGGCGC	ACAGGTGGTC	AAATCAACCA	CCAAACTGGG	300
CTAACACAC	GCCCTGGCG	CGGGGACCG	CATCGTCATC	GATCCCAACCG	GTGTCGTGTT	360
GACCAACAA	CACGTGATCG	CGGGCGCCAC	CGACATCAAT	GCCTTCAGCG	TGGCTCCCG	420
CCAAACCTAC	GGCGTCGATG	TGGTCGGGTA	TGACCGCACC	CAGGATTCG	CGGTGCTGCA	480
GCTGGCGGT	GGCGTGGCC	TGCGCTCGG	GGCGATCGGT	GGCGGCCTCG	CGGTGGTGA	540
GCCCGCTGTC	GCGATGGCA	ACAGCGCTGG	GCAGGGCGGA	ACGCCCCGTG	CGGTGCTCTGG	600
CAGGGTGGTC	GGCGTCGGCC	AAACCGTGA	GGCGTCGGAT	TCGCTGACCG	GTGCGGAAGA	660
GACATTGAC	GGGTTGATCC	AGTTCGATCG	CGCAATCGC	CCCGTGTATT	CGGGCGGGCC	720
CGTCGTCAC	GGCTTAGGAC	AGGTGGTCG	TATGAAACAGC	GCCGCGTCG	ATAACTTCCA	780
GCTCTCCAG	GGTGGGCAAG	GATTGCGCAT	TCCGATCGG	CAGGCGATGG	CGATCGCGG	840
CCAAATCCGA	TGGGGTGGG	GGTCACCCAC	CGTTCTATAC	GGGCTTACCG	CCTTCTCGG	900
CTTGGGTGTT	GTGACACACA	ACCGCAACCG	CGCACGAGTC	CAACGGCTGG	TGGGAGGGC	960
TCCGGCGGA	AGTCTCGGC	TCTTACACGG	CGACGTGATC	ACCGCGTCG	ACGGGCGTC	1020
GATCAACTCG	GGCACCGGA	TGGCGGACCG	GTTAACCGG	CATCATCCCG	GTGACGTCA	1080
CTCGTGTGAA	TGGCAAAACCA	AGTGGCGGC	CACCGGTAC	GGAAACCTGA	CATTGGCCGA	1140
GGGACCCCGC	GCTGTATTG	TGCGGATAC	CACCCCGCCG	CGGGCCATT	GGATTTGGCG	1200
CAGCGGTAT	TGGCGCTGTA	GGCCCCGAGT	TCCGTCCTCG	GTGCGGTG	CATTGTTGGA	1260
GCAATGAAACG	AGGCAACAA	CGACGGTGTG	CACCTTCCCG	TGAGGGCAG	TTACGTCGAA	1320
GGCGGTGTGG	TGAGGACATCC	GGATGCGGCA	GACTTCGGCA	CGCCGCCCGC	CTTGCCCCCG	1380
GATCGGACCT	GGTTTAAGCA	CGCCGCTTC	TACGAGGTGC	TGGTCGGG	GTTCCTCGAC	1440
GCCAGGGCG	ACGGTTCCGN	CGATCTCGT	GGACTCTACG	ATGCCCTCGA	CTACCTGAG	1500
TGGCTTGGCA	TGACTGTCAT	CTGTCGGCG	CGTTCTCTACG	ACTCACCGCT	GGCGGACGGC	1560
GTTTACGACA	TTCCGGACTT	CTAACAGGTG	TCGGCCGAGT	TCGGCACCGT	CGACGATTTC	1620
GTCCGGCTTG	TGCAACACCG	TCACCGGCA	GGTATTCGCA	TCACTACCCG	CTTGGTGTAG	1680
ATACACACT	CGGAGTACCT	CCCTCTTGT	CAGGAGTCCC	GGCCGACCC	AGACGGACCG	1740
TACGGTGA	ATTACGTGTG	GAAGCAGACCC	AGCGAGGCGT	ACACCGACG	CCGGATCATC	1800
TTCGTGTGACA	CCGAAGAGTC	GAACGGTGTCA	TTCGATCTGTG	TCCGGCGACA	GTINACTACTG	1860
GCACCGATTCTT						1872

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTTCGCCGAA	ACCTGATGCC	GAGGAACAGG	GTGTCCTCGGT	GAGCCCGACG	GCGTCGACCC	60
CGCCGCTCT	CGGGCAGATC	AGGCAGTCGC	TCTGATGGCAC	AAAAGGGTTG	ACCAAGGGTGC	120
ACGTAGCGGT	CGGAACACCC	GGGAAAGCTC	ACAGCTTGT	GGGTATTAC	AGTGGCGATG	180
TCGACCTCG	GGCCATATTCC	CTGCGCCGA	AGGGCGTATG	CATCTACAC	GACGAGCAGG	240
GTGTCCTCG	TCGGGTACAA	GGGGACACAA	TCTCGTGA	ACTGTTGAC	GACTGGAGCA	300
ATCTCGGCTC	GATTTCTGAA	CTGTCATC	CACCGCTGT	CGATCTCGC	GCTGGGGTGA	360
CGCAGCTGTC	GTCCGGTGT	ACGAACTCC	AAGCGCAAGG	TACCGAAGTG	ATAGACGGA	420
TTTCGACCC	CAAATACCC	GGGACCATCC	CCGGCAGGTC	TGCAAGATG	CTTGATCTCG	480
GGCCCAAGAG	TGCAAGGGCG	GGACCCGTGT	GGATTCGCGCA	GGACGGCTCG	CACCACTCG	540
TCCGAGCGAG	CATCGACCTC	GGATCCGGGT	CGATTCAGCT	CAACGAGTC	AAATGGAAACG	600
AACCCGCTAA	CGTCGACTAG	GCCGAAGTGTG	CGTCGACCGC	TTGCTGAAA	CGCCCTGTGTG	660
AACGGTGTCA	ACGGCACCCG	AAACATGACCC	CCCTGACCGC	ATCTGAAAT	TGACCCCTTA	720
GACCGGGCGG	TTGGTGGTTA	TTCTTCGGTG	GTTCGGCTG	GTGGGACCGC	GCCGAGGTG	780
CGGTCTTGTG	GCCGGTAGCT	GTGCCCTTGTG	AGGGCGACGA	CTTCAGCATG	GTGGACGAGG	840

CGGTCGATCA	TGGCGGCAGC	AACGACGTCG	TCGCCGCCGA	AAACCTCGCC	CCACCGCCG	900
AAGGCCTTAT	TGGACGTGAC	GATCACTG	GGCCGCTAT	ACCGGGAGGA	CACCACTGG	960
AAGAAAGAGGT	TGGCGGCCTG	GGGCTCAAAC	GGAATGTAAAC	CGACTTCGTC	AACCCACCG	1020
AGCGGATAGC	GGGCAAAACCG	GGTAGTTCG	GGGTAGATGC	GCCCCGGCTG	GTGAGCCTCG	1080
CGGAACCGTG	CTACCCATTC	GGCGGGCGTG	GGGAACAGCA	CCCGATGACC	GGCCTGACAC	1140
GCGCTATCG	CCAGGGCGAC	CGCAAGATGA	GTCTTCCCGG	TGGCAGGCCG	GGCCCCAAAAA	1200
CACGACGTTA	TCGCGGGGG	TGATGAATC	CAGGGTGCCTC	AGATGTGCGA	TGGTGTGCGG	1260
TTTGGAGGCCA	CGAGCATGCT	CAAAGTGCRA	CTCTTCAC	GACTTCCGAA	CCGGGAAGCG	1320
GGCGCGCCGG	ATGCGGCCCT	CACCGATG	GGACTTCCGG	GCTGACACTT	CCCGCTGCG	1380
GCAGCGGGCC	AGGTATTC	CGTGGCTCA	GTTCCTCGG	CGGGGGCGAT	CGGCCACCG	1440
GGACACTGAC	TCACCGAGGG	TGGGAGCTTT	CAATGCTCTT	GT		1482

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTCCGGCA	CGAGCCGGCG	ATAGCTTCTG	GGCCGCGGGC	GACAGAGATGG	CTCGAGGGTT	60
CGTGTCTGGG	GGCACCCGGC	GGCACCACAC	CCTGACCGGT	GAGGGCTCTG	AAACACGGCA	120
CGGTCACTCG	TTGCTGTCTG	ACGCCACCA	CCCGGGCGTG	TTGCTCTAG	ACCCGGCTT	180
CGCCATCGAA	ATCGCTTACCA	TGCGNAGGAA	CGGACTGGCC	AGGATGTGCG	GGGAGAACCC	240
GGAGAACATC	TTCTTCTAC	TCACCGCTCA	TCACAGCGC	TACGTGCGAC	CGCCGGAGCC	300
GGAGAACATTG	GATCCCGAGC	CGCTGTGGG	GGGTATCTAC	CGNTATCACG	CGGCCACCGA	360
GCAAGGCACC	AACAGGNGC	AGATCTCGG	CTCCGGGGTA	GCGATGCCCG	CGGGCGTCTG	420
GGCAGCACRG	ATGCTGGCCG	CCGAGTGGGA	TGTCGCCGCG	GACGTGTGGT	CGFTGACCCAG	480
TTGGGGCAG	CTAACACCGG	ACGGGGTGGT	CATCGAGACC	GAGAACGTC	GCCACCCCGA	540
TCGGCGGGGG	GGCGTGTCCCT	ACGTGAGGAG	ACGGCGGGAG	ATGCTCGGG	GCCGGGTGTAT	600
CGCGGTGTG	GACTGGATGC	CGCGGGTCC	CGAGCAGATC	CGACCGTGGG	TGCGGGCAC	660
ATACCTCAGC	TTGGGACCGG	ACGGGTTCCG	TTTTCCGAC	ACTGGGGCG	CCGGTGTCTG	720
TTACTTCAC	ACCGACGCCG	AACTCCAGGT	TGGTCGCGGT	TTTGGGAGGG	TGTTGGCCGGG	780
TCGACGGTGTG	AATATCGACC	CATTGGTGC	CGGTCTGGG	CGGCCGCC	AGTTACCCGG	840
ATTCGACGAA	GGTGGGGGGT	TGCGCCGAGAN	TAAGTT			876

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1021 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCCCCCGG	GCTGGCAGGAA	TTCCGGCAGA	GAGACAAAAT	TCCACCGGTT	AATGCAAGGAA	60
CAGATCCATA	ACGAATTCAC	AGCGGCACAA	CAATATGTCG	CGATCGCGGT	TTATTCGAC	120
AGCGGAAGACC	TGCCCGAGTT	GGCGAAGCAT	TTTTACGAC	AAGCGGTGCA	GGAAAGAAC	180
CATGCAATGA	TGCTCGTGC	ACACCTGTC	GACCGGGACG	TTCGTGTGCA	AATTCCCGC	240
GTAGACACGG	TGCGAACAAA	GTTCGACAGA	CCCGCGGAGG	CACTGGCGT	GGCGCTCGAT	300
CAGGAACGCA	CAGTCACCGA	CGACGGTGTG	CGCTGTGACAG	CGGTGGCCCG	CGACGAGGGC	360
GATTTCCTCG	GCGAGCAGTT	CATGAGTGG	TTCTTGCGAG	AACAGATCGA	AGAGGTGCC	420

TTGATGGCAA	CCCTGGTGCG	GGTTGCCGAT	CGGGCCGGGG	CCAAACCTGTT	CGAGCTAGAG	480
AACTTCGTCG	CACGTGAAGT	GGATGTGGG	CCGGCCGCAT	CAGGGCGCCC	GCACGCTGCC	540
GGGGGCCGCG	TCTAGATCCC	TGGGGGGAT	CAGCGAGTGG	TCCCGTTGCG	CCGCCCCGCTC	600
TCCAGCCAGG	CCCTGGTGCG	GGCGGGGTGG	TGAGTACCAA	TCCAGGCCAC	CCCGACCTCC	660
CGGNAAAGT	CGATGTCTC	GTACTCATCG	ACGTTCCAGG	AGTACACCGC	CCGGCCCTGGA	720
GCTGCCGAGC	GGTCAACGAG	TTGCGGATAT	TCCCTTAACG	CAGGCAGTGA	GGGTCCACG	780
GGCGTTGGCC	CGACCCCGT	GGCCCACTG	CTGGTCAGGT	ATCGGGGGGT	CTTGGCGAGC	840
AAACAACCTG	GCAGGAGGGG	TGGAGCCCGC	CGGATCCCA	GACCGGGGGG	GGCAAACAGA	900
CATCAACACC	GCACGGGATC	GATCTGCGGA	GGGGGGTGCG	GGAAATACCGA	ACCGGTGTAG	960
GAGGCCAGC	AGTTGTTTT	CCACCAAGCGA	AGCGTTTCTG	GGTCATCGGN	GGCNNTTAAG	1020
T						1021

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGTGCCGACG	AACGGAAGAA	CACAACATG	AAGATGGTGA	AATCGATCGC	CGCAGGTCTG	60
ACCGGGCCGG	CTCGAATCGG	CGCCGCTGCG	CGCCGGTGTGA	CTTCGATCAT	GGCTGGCGGN	120
CCGGTCGTAT	ACCAAGATGCA	GGCGGTGCGT	TTCGGCGGCC	CACTGCGTT	GGACCCGONA	180
TCCGCCCTG	ANGTCCGAC	CGCCGCCAG	TGGACCAAGNC	TGCTAACAG	NCTCGNCGAT	240
CCCAAACGTG	CGTTGNGAA	CAAGGGNAGT	CTGGCTGAGG	GNGGNATCGG	NGGNANCAGG	300
GGNGNGNATC	GNCGANCACAA					321

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TCTTATCGGT	TCCGGTTGGC	GACGGTTTT	GGGNCGGGGT	GGTTAACCCG	CTCGGCCAGC	60
CGATGACCG	CGCGCGGAGAC	GTCGACTCGG	ATACTCGGG	CGCGCTGGAC	CTCCAGGCC	120
CCTCGGTGT	GNACCGCCAA	GGCGTGAAGG	AGCCGTTGNA	GACCGGGATC	AAGGGCATTTG	180
ACGGCATGAC	CCCGATCGC	CGCGGGCAGG	CGCACGCTGAT	CATCGGGGAC	CGCAAGACCG	240
GCAAAACCG	CGGTCTGTGT	CGGACACCAT	CCTCAAACCA	GCGGGAAGAAC	CTGGGAGTCC	300
GTTGGATCCC	AAGAAGCAGG	TGGCCTTGTG	TATACGTTGG	CCATCGGGCA	AGAAGGGGAA	360
CTTACCATCG	CGG					373

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTGACGGCGT GATGGGATTG	CTGGGGGGGG	CCGGTCCCGT	GGCGGTGGTG	GATCAGCAAC	60	
TGGTACCGG	GGTGGCCCAA	GGCTGGTCTG	TGCTCAGGC	AGCCGCTGTG	CGGGTGGTGT	120
TCTTGACCGC	CTGTTACCGG	TGGCCGAGAT	TAAGCGAGAT	CAAGGCGGGC	GAATCGGTGC	180
TGATCCATGC	CGGTACCCGC	GGTGTGGGCA	TGGCGCTGT	GCAGCTGGCT	CGCCAGTGGG	240
GCGTGGAGGT	TTTCGTCRCC	GCCAGCCGTG	GNAAGTGGGA	CACGCTGGGC	GCCATNGNGT	300
TTGACGACGA	NCCATATCGG	NGATCCCCNC	ACATNCAGAAG	TTCCGANGGA	GA	352

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAAATCCCG	TTCATTCCGT	TCGACCAGCG	GCTGGCGATA	ATCGACGAAG	TGATCAAGCC	60
GCGGTTCCG	GGCTCATGAG	GTCAACAGGA	GTAAATCAGCA	AGTTCTCTGG	TATATCGCAC	120
CTAGCGCTCA	GTGCTTGCG	AGATCGCTT	CGTACCGCTCA	TGCCATGTAC	CGGTTCCGGT	180
GCCGCAGCTG	CATGTCGGG	GGCTGCATCG	TGGCCACCGG	TGTGGCGGGT	CTCGGGGTCG	240
GGCGCAGCTG	CGCCAGCGGA	ACCGCCGGG	TGCCCCGACTA	CTACTGGTGC	CCGGGGCACG	300
CTTCGACCC	CGCATGGGG	CCCAACTGGG	ATCCCTACAC	CTGCCATGAC	GACTTCCACC	360
GCGGACCGA	CGGGCCCGAC	CACACCGGG	ACTACCCGG	ACCCATCTC	GAAGGTCGGC	420
TGCTTGACGA	TCCCCTGGT	GGCGCCGGC	CCCCGGCTGC	CGGGGGCGC	GCATAGCGT	480
CGTTGACCGG	GGCGCATCAG	CGAACATCGG	TATAAACCGG	GGCGTGGCCC	CGGCAAGCTA	540
CGACCGCCGA	CGGGGAGAT	TTACGCTCC	GTGCGATGG	ATCGCCCGT	CCGATGACAG	600
AAAATAGGCG	ACGGTTTTGG	CAACCGCTTG	GAGGACGCTT	GAAGGGAAAC	TGTCATGAAAC	660
GGGCACAGCG	CCTCCACCAT	CGACATCGAC	AAGGTTGTTA	CCCGCACACC	CGTTCCGGG	720
ATCGTG						726

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CGCGACGACG	ACGAAACGTCG	GGCCCACCAAC	CGCCTATGCG	TTGATGCAGG	CGACCGGGAT	60
GGTCCGGAC	CATATCCAAG	CATGCTGGT	GGCCACTGAG	CGACCTTTG	ACCGCCGGG	120
CTGCCGATG	CGGGCCCGGT	GAAGTCATG	CGCCGGGGT	TGTGACCTG	ATGAAACCGA	180
ATAGGGAACA	ATAGGGGGGT	GAATTGGC	TTCATATGCG	GGTATGGCTG	GAATCCAT	240
GGCGGGCAT	GCTCGGGCC	GACCAAGCTC	GGCGAGCGG	GCCAGCCGA	ATCTGGAGGG	300
AGCACTCAAT	GGCGGGCGATG	AAGCCCGGA	CCGGCACCGG	TCTTTGGAA	GCAACTAAGG	360
AGGGCGCCG	CATTGATGAT	CGATGACAC	TTGAGGGTGG	CGGTGCGCTG	GTGCTGAGC	420
TGACACCGGA	CGAACGGCC	GCACTGGTC	ACGAACCAA	AGGGCTTACT	AGCTAAAGACC	480
AGCCCAACGG	CAGATGGTCG	CGCTTACGG	CACACCTTCC	GGTAGATGTC	CAGTGTCTGC	540
TCGGCGATGT	ATGCCACCGA	GAACCTTGG	ATACAGCGCT			580

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AACGGAGGCG CGGGGGTTT TGGCGGGGCC GGGCGGTTG GCGGCAACGG CGGGGCCGGC	60
GGTACCGGCC CGGTGTTCCG TGTCGGGGG GCGCGTGCGG CGCGAGGCAA CGGCATCGCC	120
GGTGTACCGG GTACGTCGGC CAGCACACCG GGTGGATCCG	160

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GACACGGATA CGATGGTGT GTACGCCAAC GTTGTGCGACA CGTCGAGGC GTTCACGATC	60
CAGCGCACAC CCGACGGCGT GACCATCGGC GATGCGGCC CGTTCGCGGA GGCAGCTGCC	120
AAGGGCATGG GAATCGACAA GCTGGGTTA ATTCTACCG GAATGGACCC GTCGCTGCT	180
GAACCGGAAAC AGTGGGACCGA CGGCAACACG ACGTGGGCGT TGGGGCCCGG TGTCGTTGTC	240
GCCTACGAGC GCAACGTACA GACCAACGCC CG	272

## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCAGCCGGTG GTTCTCGGAC TATCTCGGCA CGGTGACCGA GCGCGACCTG CGCGAGCTGA	60
ACGGGATCGA CGACAGCGAT CGCTCGGCCG GGTTCATCGC CTACCTGCGC GCTATCACCG	120
CGCAGGAGCT GAACGTGGCC GAAGCGGCCG GGGTCATCGG GGTCGACCGG GGGACGATCC	180
GTTCGGATCT GGCGTGGTTC GAGACGGTCT ATCTGGTACA TCGCCTGCCG GCCTGGCTGC	240
GGAAATCTGAC CGCGAAAGATC AAGAAGCGGT CAAAGATCCA CGTCGTCGAC AGTGGCTTCG	300
CGGCCCTGGTT CGCCGGG	317

## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GATCGTGGAG	CTGTCGATGA	ACAGCGTTGC	CGGACCGCGC	GCGGCCAGCA	CGTCGGTGT	60
GCAGCGCCGG	ACCACCTCGC	CGGTGGCAG	CATGGTGTATG	ACCACGTGG	CCTCGGGCCAC	120
CGCTTCGGC	GCGCTACGAA	ACACCGCGAC	ACCGTGCAGC	GCGGCCGCGG	ACGCCGCGGT	180
GG						182

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GATCGCGAAG	TTTGGTGAGC	AGGTGGTGC	CGCGAAAGTC	TGGGCGCTG	CGAAGCGGGT	60
CGGGGTTCAC	GAGGGCGAAGA	CA CGCCTGTC	CGAGCTGCTG	CGGCTCGCT	ACGGCGGGCA	120
GAGGTTGAGA	TTGCCCGCCG	CGCGGAGCCG	GTAGCAAAGC	TTGTGCGCGT	GCATCCCTAT	180
GAGACTCGG	GGTTAGGCAT	TGACCATGGC	GTGTACCGCG	TGCCCGACGA	TTGGACGCGT	240
CCGTTGTCAG	ACGACGTGCT	CAACCGCTTT	CACCGGTGAA	CGCGTACCTC	ATCGACACCC	300
ACGTTTGG						308

## (2) INFORMATION FOR SEQ ID NO:31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCGACGACGA	GCAACTCACG	TGGATGATGG	TCGGCAGCGG	CATTGAGGAC	GGAGAGAAC	60
CGGCCGAAGC	TGCGCGCCGG	CAAGTGTCA	TAGTGAACGG	CCGTAGAGGG	CTCCCCCGAT	120
GGCACCGGAC	TATTCTGGTG	TGCGCTGGC	CGGTAAAGAC	GGGTAAAGA	ATGTGAGGGG	180
ACAGGATGAG	CAATCACACC	TACCGAGTGA	TGGAGATCGT	CGGGACCTCG	CCCGACGCCG	240
TCGACGCCGC	AATCCAGGGC	GGTCTGG				267

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTCGTGGCGA	AAGAATGTGA	GGGGACACGA	TGAGCAATCA	CACCTACCGA	GTGATCGAGA	60
TCGTCGGGAC	CTCGCCGAC	CGCGTGCAGC	CGGCATCCA	GCGCGCTG	GCCCGAGCTG	120
CGCAGACCAT	CGCCGGCTG	GA CTTGCTCG	AA GTACAGTC	AATTGAGGC	CACCTGGTGC	180
ACGGGAGCGGT	CGCGCACTTC	CAGGTGACTA	TGAAGATCG	CTTCCCGTGG	AGGATTCCTG	240
AACCTTCAAG	CGCGGCGCAT	AACTGAGGTG	CATCAAG	CGACTTTCC	AGAACATCTT	300
GACGGCGCTG	AAACCGGGTT	CGACGGCGG	TGGCTCCGCC	GAGGGCGTGC	CTTCCAAAATC	360
CCTGCGACAA	TTCGTGGCG	CGCCTACAA	GGAAAGTCGGT	GCTGAATTG	TCGGGTATCT	420

GGTCGACCTG	TGTGGGCTGC	AGCCGGACGA	AGCGGTTGCTC	GACGTCGGCT	GCGGCTGGG	480
GCGGATGGCG	TGTCGGCTCA	CCGGCTATCT	GAACAGCGAG	GGACGCTACG	CCGGCTTCGA	540
TATCTCGCAG	AAAGCCATCG	CGTGGTGGCA	GGAGCACATC	ACCTCGGGC	ACCCCACTT	600
CCAGTTGAG	GTCTCCGACA	TCTACAACTC	GCTGTACAAAC	CCGAAAGGGGA	AATACCACTC	660
ACTAGACTTT	CGCTTCCCAT	ATCCGGATGC	GTGCGTTGCG	GTGGTGTTC	TTACCTCGGT	720
GTTCACCCAC	ATGTTTCCCG	CGGACGTGGA	CGACTATCTG	GACGAGATCT	CCCGCGTGTCT	780
GAAGCCGGC	GGACGATGCC	TGTGCACGTA	CTTCTTGCTC	AATGACGAGT	CGTTAGGCCA	840
CATCGGGAA	GGAAAGAGT	CCACAACTG	CGACGATGAG	GGACCGGGTT	ATCGGACAAAT	900
CCACAAAGAG	CGCCCGGAG	AACGAACTCG	CTTGCGGAG	ACCTTCTGCA	GGGATGCTCA	960
TGGCAAGTT	GGCCTCGCCG	TGACGAACC	ATTGCACTAC	GGCTCATGGA	GTGGCCGGGA	1020
ACCACGCCCTA	AGCTTCAGG	ACATCGCAT	CGCGACCAA	ACCGCGAGCT	AGGTGCGCAT	1080
CCGGGAAGCA	TGCGCACATC	GTGGCGCCGA	GGCGCGCTGC	CGGGCAGGGCG	ATTAGGGCGG	1140
CAGATTAGCC	CGCGCGGCT	CCCGGCTCCG	AGTACGGCG	CCCGAATGGC	GTCACCGGCT	1200
GGTAACCAACG	CTTGGCGCCG	TTGGGGCGCG	CTTGGCGGAT	CAGGTGGTAG	ATGCGGACAA	1260
AGGCTGGGTG	ATTCGGTCATC	ACCAACGGCT	ACAGCAGCG	GTGTTGCAAC	AGGCCGAACG	1320
CCACCCCCGT	CTCCGGGTCT	GTCCAGCCGA	TCGAGCCGCC	CAAGCCACAA	TGACCAAAAC	1380
CCGGCATC	GTGGCCATGC	GGCATACTCGT	ATGACGAGT	ATGAAAATT	AAGGGCACCA	1440
ATAGATTTCG	ATCCGGCAGA	ACTTGGCGTC	GGTGGGGGT	CAGGGCCGTG	ACCAGCTCCC	1500
GGACAAAGAA	CCGTATGCCG	TCGATCTCGC	CTCGTGC			1539

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTGCAGGGTG	GCGTGGATGA	GCGTCACCGC	GGGGCAGGCC	GAGCTGACCG	CCGCCAGGT	60
CCGGGTTGCT	ACGAGACGGC	GTATGGGCTG	ACGGTGC	CCGGGTTGAT	120	
CGCGGAAGAC	CAGTGTGAAAC	TGATGATTC	TGATGGGAC	AACCTCTTG	180	
CCCGCGATC	CGCGTCACAG	AGGCCGATA	CGGCAGATG	TGGGCCAAG	240	
GATGTTGCG	TACCGCCGGG	CGCGGACGCC	GGCGACGGCG	ACGTTGCTG	300	
GGGCCCGGAG	ATGACGACCG	CGGGTGGGCT	CTTCGAGCG	GGCCGGCGG	360	
CTCCGACACC	GCCGCGGCGA	ACCAGTTGAT	GAACAATGTG	CCCCAGGCC	420	
GGCCCGACCC	ACGCAGGCCA	CCACGCCCTC	TTCCAACTG	GTTGGCTGT	480	
CTCGCGCAT	CGGTGCGGCA	TCAGCACATC	GGTGTGCGAT	GCCAAACAA	540	
GACCAACTCG	GGTGTGCGA	TGACCAACAC	CTTGAGCTCG	ATGTTGAAGG	600	
GGCGGCCGCC	GGCGGCCGCC	TGCAACACCG	GGCGCAAC	GGGGTCCGGG	660	
GCTGGGCAAC	TGCGTGGGCT	CTTGGGGCT	GGGGCGTGGG	GTGGCCGCCA	720	
GGCGGCCCTCG	GTACGGTAG	GTACCGGGA	TGGCGAAA	TATGCAAGT	780 <sup>1</sup>	
GAACGGTGTT	CCGGCGTAA	GTTCACCCCC	GTTCACCTGGA	TGCGGTGAAC	840	
GAACAGCTTA	C				851	

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GATCGATCGG	GGGGAAATT	GGACCA	GATT	CGCCTCCGGC	GATA	ACCCAA	TCAATCGAAC	60
CTAGATT	TTCGTC	TCAGG	GGCCGAGTA	ATGGCTCGCA	GGAGAG	GAAC	CTTACTGCTG	120
CGGGCAC	TCG	TCGAGGTCC	TCGATACGGC	GGAA	AGGC	GTC	GACATT	180
CCATCCA	AC	GTTCGAGGGC	CACTCCAGCT	TGTGAG	GGAG	GCGAC	GAGT	240
GCTTGGTCAA	GATC							254

## (2) INFORMATION FOR SEQ ID NO:35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GATCCTGACC	GAAGCGCCG	CGGCCAAGG	GAAGTCGCTG	TTGGACCA	AGGGACGGG	AGGGACGGG	60
CGATCTGGGG	CTCGCGATCG	CGGTTCA	GGGGGGTGC	GCTGGATTG	GCTATAACCT		120
TTCCTCTGAC	GACCGGAGCC	TGGATGTTGA	CCAAACCGCG	GAGTTCGGTG	GTGTCAGGTT		180
GATCTGGGAC	CGGATGAGCG	CGGGCTATGT	GGAA	GGCCGCG	TCGATCGATT	TCGTCGACAC	240
TATTGAGAAG	CAAGGTTAC	CATCGACAA	CCAAACGCGA	CCGGCTCTG	CGCGTCGCGG		300
GATTGCTCA	ACTGATAAAA	CGCTAGTACG	ACCCCGG	GGC	CAACACCC	TACGACCA	360
CCAAGACCTG	ACCGCGCTGG	AAAGGCAACT	GAGGCGATGCC	TTGAC	CTGCGGCG		420
GGCCGCGGCG	GGCAGGGTGC	ACCTGCA	TGAA	CAGCAC	CTGGGCGCTG	TATTGCGACC	480
AGTACACGAT	TTTGTGATC	GAGTCGATC	CGACCTGGG	GA	ACTGCTT	CGGAACGGGT	540
CGCTGCTCAG	TTTGTGCA	GGCTGATCGG	AGCGCTTGT	CGC	ACCGCG	TCTGGA	600
CGCACAGCGC	ATTGCGAACG	ATGGTGTCA	CATCGCGGTT	CTCAGCGCG	TTGAGG	TATC	660
CTCTGAATCGC	GGTTTTGGCC	GGTCCC	AAAGTGTGCC	TGCGGTGTTG	GT	CCGTTGG	720
TGCGGACCCC	GTATGATGAC	GGCGCGCTCA	TAGGCC	ACAC	CAGGGCGAGG	GCTAACACAA	780
TGCCGATCA	CAGCGCTT	TGCGTCGCT	TCGGG	TAGGA	CACCTGCGGC	GGCACGCGG	840
GATATCGGG	GGGGCGGAGC	GGCGCGCTGT	CTGGCG	TCC	CGGGGCGAG	GGGGGTTCCG	900
CGGC	GGG	TAGTCCAGGG	CTTGGG	GTGGG	GTGGGATGAG	GGCTCGGGGT	960
ACGGCGCCGG	TCCGTTGGTG	CCGACACCGG	GGT	TGGG	GGGACCG	GGCAT	1020
TTCCTCTAGG	TTGTTGAGC	GGACCGCTG	TA	GGGG	GGGACCGGT	CGCGTCAGCC	1080
GGCAGCATCG	GCAATCAGGT	GAGCTCTTA	GGCAGGCTAG	CGCA	ACACGCT	GCCGTCAGCT	1140
CTCAACCGCA	CGGGCGGGC	CGCGCGCCCG	ATAATGTTGA	AAGACT	AGGC	AACCTTAGGA	1200
ACGAAGGAGC	GAGATTTGT	GACGATC					1227

## (2) INFORMATION FOR SEQ ID NO:36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGCGGTGTCGG	CGGATCCGGG	GGGTGGTGA	ACGGCAACGG	GGGGCGCCG	GGGGCGCCG	60	
GGACCGCGCG	TAACGGTGT	GGCGCGCGCA	ACGCTGTT	GTTCGGG	GGCGGGTCCG	120	
GGCGNGCCGG	CACCAATGGT	GGNGTCCGCG	GGTCCGGCGG	ATT	TGCTAC	GGCAACGGCG	180
G							181

## (2) INFORMATION FOR SEQ ID NO:37:

(1) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 290 base pairs	60
(B) TYPE: nucleic acid	120
(C) STRANDEDNESS: single	180
(D) TOPOLOGY: linear	240
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:	290
GCGGTGTCGG CGGATCCGGC GGGTGGTTGA ACGGCACAGG CGGTGTCGGC GGCGGGGGCG	60
GCGACGGCTT CTTTGGCGGT GCGGGGGGCC AGGGCGGCC CGGTGGGAG GGCGGCAATG	120
GCGCGGCTC AACCAGGGC GGGCGGCC CGGTGGTGGC GGAGGCAACG	180
CCCCGGACGG CGGCTTCGGT GGCACAGGGC GTAAGGGTGG CCAGGGCGGN ATTGGCGCG	240
GCACTCAGAG CGCGACCCGC CTCGGNGGTG ACGGCGGTGA CGGCGGTGAC	290
(2) INFORMATION FOR SEQ ID NO:38:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 34 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:	
GATCCAGTGG CATGGNGGTG GTCAGTGGAA GCAT	34
(2) INFORMATION FOR SEQ ID NO:39:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 155 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:	
GATCGCTGCT CGTCCCCCCC TTGCCGCGGA CGCCACCGGT CCCACCGTTA CGAACAAAGC	60
TGGCGTGGTC GCCAGCACCC CGGGCACCGC CGACGCCGGA GTCGAACATT GGCAACCGTC	120
TATCCCCACC ATTGCCCGG GNCCCCACCGG CACCG	155
(2) INFORMATION FOR SEQ ID NO:40:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 53 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:	
ATGGCGTTCA CGGGGCCCGG GGGACGGGGC AGCCCGGNGG GGCGGGGGGG TGG	53
(2) INFORMATION FOR SEQ ID NO:41:	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GATCCCCACGC GGGTGCAGAC GGTGCCCCCG GCGCCACCCC GACCAGCGC GGCAACGGCG	60
GCACCGCGG CAACGGCGC AACGCCACCG TCGTGCGNGG GGCCGGCGGG GCCGGCGCA	120
AGGGCGGCA CG	132

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GATGGCGGC CGGNACGGNC GGGGACGGCG GCAAGGGCGG NAACGGGGC GCGGNAGCCA	60
CCNGCCAAGA ATCTCCGNG TCCNCCAATG GCGCAATGG CGGACAGGGC GGCAACGGCG	120
GCANCGCGG CA	132

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CGGCACGGAGG ATCGGTACCC CGGGCATCG GCAGCTGCCG ATTCGCCGGG TTTCCCCACC	60
CGAGGAAAGC CGCTTACCAAGA TGGCGCTGCC GAAGTAGGGC GATCGCTTCG CGATGGGGC	120
ATGACGGGGC GGCATCAATAT TAGTGCAGGA ACCTTTCAGT TTAGCGACGA TAATGGCTAT	180
AGCCTAAGG AGGATGATCC GATATGAGC AGTGCAGAC CGTGACGGTG GATCAGCAAG	240
AGATTTGAA CAGGGCAAC GAGGTGAGG CCCCAGATGCC GGACCCACCG ACTGATGTC	300
CCATCACACC GTGGCAACT ACGGGNGNTA AAAACGCCCG CCAACAGNTG GTNTTGTCCG	360
CCGACAAATC GCGGGAAATAC CTGGCGGCCG GTGCCAAGA GCGGCAGCGT CTGGCGACCT	420
CGCTGCGCAA CGCGGCCAAG GNGTATGGCG AGGTTGATGA GGAGGCTGCC ACCGGCTGG	480
ACAACGACGG CGAAGGAAGT GTGCAGGCAG AATGGCCCGG GGGCGTCCGG GGGGACAGTT	540
CGGCCGAAACT AACCGATACG CCGAGGGTGG CCACGGCCGG TGAACCCAAAC TTCACTGGATC	600
TCAAAGAAGC GGCAAGGAAG CTCGAACAGG GCGACCAAGG CGCCTCGCTC GCGCACTGNG	660
GGGATGGTG GAACACTTNC ACCCTGAGCG TGCAAGGCGA CG	702

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

## (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAAGCCGCAG CGCTGTCGGG CGACGTGGCG GTCAAAGCGG CATCGCTCGG TGGCGGTGGA	60
GGCGCGGGGG TCCCGTCGGC GCCGTTGGGA TCCGCGATCG GGGGCGCCGA ATCGGTGCGG	120
CCCGCTGGCG CTGGTGACAT TGCCGGCTTA GCCCAGGAA GGGCGGGCGG CGGGCGCCCG	180
CTGGCGCGGC GTGGCATGGG AATGCCGATG GGTGCCGCGC ATCAGGGACAA AGGGGGCGCC	240
AAGTCCAAGG GTTCTCAGCA GGAAGACGCA GGCGCTCTAA CGCAGGATCC TCAGTGCAG	298

## (2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CGGCACGAGG ATCGAATCGC GTCGCCGGGA GCACAGCGTC GCACTGCACC AGTGGAGGAG	60
CCATGACCTA CTCGCCGGGT AACCCCGGAT ACCCGCAAGC GCAGCCCGCA GGCTCTCTACG	120
GAGGGCTCAC ACCCTCTTC GCCCCACGCCG ATGAGGGTGC GAGCAAGCTTA CGCATGTAC	180
TGACATCGC GGTTGCGATG CTGGCTCTGG CTGGCTACTT CGCCAGCTTC GGGCCAAATGT	240
TCACCCCTAG TACCGAATC GGGGGGGGGT ATGGCCGACT GTCCCGGTGAC ACTGGGTGTC	300
CGGGCGGGGT GGCTGCTGCTG GCTGCGCTGGT TTGCGGGGGT GTTCTGGTG CCTAAGGCCA	360
AGAGCCATGAC GACGGTAGTTT GCGGTGCTCC GGGTACTCGG CGTATTCTCG ATGGTCTCGG	420
CGACGTTAA CAAGCCACG GCCTATTGCA CGCGTGTGGGC ATTGTGGGTT GTGTGTTGGCTT	480
TCATGCTTT CCAGCGGGGT GCGCGAGTCC TTGGCCTCTT GTTGGAGACCC GGCGCTATCA	540
CCGGCCCGC GCCCCGGCCC AAAGTCCGAC CCTATGGACA GTACGGCGG TACGGGCAGT	600
ACGGGCACTA CGGGGTCSAG CGGGGGTGGT ACTACCGTCA GCAGGGTGTG CAGCAGGGCG	660
CGGGACTCCA GTCCGCGCCG CCGCAGCAGT CTCCGCGACCC TCCCAGGATAT GGTCGGCACT	720
ACGGCGGCTA TTGGCTCAGT CGGAGCCAACT CGGGCAGTGG ATACACTGCT CAGCCCCCGG	780
CCCGCCGCCG GGCGCAGTCC GGGTGCACAC AATCGACCA GGGCCCATTC AGCGCACCTA	840
CCGGCTTCCC GAGCTTCAGC CCACCCACAC CGGTCACTGC CGGGACGGGG TCCGAGGTG	900
GTTCGGCTCC AGTCAACTAT TCAACCCCCA CGGGGGGGCA CGACTCGTCG TCCCCGGGG	960
GGGCGCCGGT CTAACCGGGC GTTCCCCGGT CGCGTGCAGC GTGTGCGCGA AGAGTGAACA	1020
GGGTGTCAAGC AAGCGCGGAC GATCCTCGTG CGCAATTTC	1080

## (2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CGGCACGAGA GACCGATGCC GCTACCTCG CGCAGGGAGC AGGTAATTTC GAGCGGATCT	60
CGGGCGACCT GAAAACCCAG ATCGACCAAG TGGAGTCAGC GGCAGGGTTC TTGCAAGGGCC	120
AGTGGGGCGG CGCGGGGGGG AGGGCCGCC AGGCGCCGGT GTGCGCTTC CAAGAAGCAG	180
CCAATAAGCA GAAGCAGGAA CTGACGAGA TCTGACGAA TATTCTGAG GCGGGCTCC	240
AATACTCGAG CGCCGACGAG GAGCAGCAGC AGGCGCTGTC CTGCAAAATG GGCTTCTGAC	300
CCGCTAATAC GAAAAGAAAC GGAGCAA	327

## (2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CGGTGGCGAT GATGGCGTTG TCGAACGTGA CGCATTCTGT ACCGCCGTG TTGAGATCAA	60
CCAAACACGT GTTGGCGTCG GCAAATGTGC CGNACCCGTG GATCTCGGTG ATCTTGTCT	120
TCTTCATCATG GAAAGTGCACCA CGCGGCCACCC TGCCCTCGGN TACCTTTCGG	170

## (2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GATCCGGCGG CACGGGGGGT GCGGGCGGGC GCACCGCTGG CGCTGGCGGC AACGGCGGGG	60
CCGGGGGTGG CGGGCGAACCC GGTGGGTTGC TCTTCGGCAA CGGCCTGGCC GGCAGGGCACG	120
GGGCGGT	127

## (2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CGGCGGGCAAG GGCAGCACCG CGGGCAACGG GAGCGGCGCG GCGGGCGGCA ACGGCGGCAA	60
CGGCGGCTCC GGCCCTCAACG G	81

## (2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GATCAGGGCT GGCGGGCTCC GGCCAGAACGG GCGGTAACGG AGGAGCTGCC GGATTGTTTG	60
GCACACGGCGG GGCCGGNGGT GCGCGCGGT CCAACCAACG CGGTAACGGC GGNGCGGGCG	120
GAAACGGTGG TGCCGGTGGG CTGATCTGG	149

## (2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CGGCACGAGA	TCACACCTAC	CGAGTGTATCG	AGATCGTCGG	GACCTCCGCC	GACGGTGTGCG	60
ACGCGNAAT	CAAGGGCGGT	CTGGGCGCGG	CTGGCCAGAC	CATGCGGGCG	CTGGACTGGT	120
TCGAAGTACA	TCGAATCTGA	GGCCACCTGG	TGACGAGAC	GGTCGCGCAC	TTCCAGGTGA	180
CTATGAAGT	CGGCTTCGGC	CTGGAGATT	CCTGAACCTT	CAAGGGCGGC	CGATAACTGA	240
GGTGCATCAT	TAAGCGACTT	TTCCAGAACAA	TCCTGACCGG	CTCGAAACGC	GGTTCAGCCG	300
ACGGTGGCTC	CCCGGAGGGG	CTGGCTCCAA	AAATCCCTGG	ACAATTGCTG	GGCGG	355

## (2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATGCATCACCC	ATCACCATCA	CATGCATCAG	GTGGACCCCA	ACTTGCACAG	TGCGAAGGGAA	60
CGATTGGCGG	CACTGGCTAT	CGCGGGATG	GGCAAGGCCA	GCCCTGGTAC	CGTTGGCGGTG	120
CCCGCGACCG	CCAACCGCCG	TCGGGAGCCA	GGGGCCCCCGG	TACCCACAC	GGCCGCCCTCG	180
CCGCGTCTGA	CGCGTCTGAGC	GCCACCGCA	CGGGCAGACAC	CTGTTGCC	CCCACCAACCG	240
GCCGCCGCCA	ACACGGCAA	TGCCCGACCG	GGCGATCCCCA	ACGCAGACACC	TCCCGCCGCC	300
GACCGAACG	CACCGCCGCC	ACCTGTCAATT	GCCCCAAACCG	CACCCCAACCC	TGTCGGGATC	360
GACAAACCGG	TTGGAGGATT	CAGCTTCGGG	CTGCGCTGTG	GCTGGGTGGA	GTCTGACGCC	420
GCCCACTTCG	ACTACCGTTTC	AGCACTCTTC	AGCAAACCA	CGGGGGACCC	GCCATTTC	480
GGACAGCCGC	CGCGCGTGGC	CAATGACACC	CCTATGTTG	TGGGCCGCT	AGACCAAAAG	540
CTTTCACCCA	GGCGCGAACG	CACCGACTCC	AAGGCCCGGG	CCCCGGTTGGG	CTCGGACATG	600
GGTGAGTTCT	ATATGGCTCA	CCCGGGCACCC	CGGATCAACC	AGGAAACCGT	CTCGCTTCGAC	660
GCCAAAGGGG	TGTTCTGGAAAG	CGGGCTGTAT	TACGGAATCA	ATTTCAAGGGA	TCCGAGTAAAG	720
CCGAAAGGGG	AGATCTGGAC	GGGGCTTAATC	GGCTCGCCCG	CGGCGAACGC	ACCGGACGCC	780
GGGCCCTCTC	AGGGCTGTTT	TGTTGTTATGG	CTCGGGACCC	ACCAACACCC	GGTGGACAAAG	840
GGGCCGGCCA	AGGCCGCTGGC	CGAATGATC	GGGGCTTTGG	TGGCCCCGCC	GCCGGCGGCC	900
GCACCGGCTC	CTGCAAGAGCC	CGCTCCGGCG	CGGGCGCCGG	CGGGGAAAGT	CGCTCCTACC	960
CCGACGACAC	CGACACCGCA	GGGGACCTTA	CGGGCTCTGA			999

## (2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met His His His His His Met His Gln Val Asp Pro Asn Leu Thr  
 1 5 10 15  
 Arg Arg Lys Gly Arg Leu Ala Ala Leu Ala Ile Ala Ala Met Ala Ser  
 20 25 30  
 Ala Ser Leu Val Thr Val Ala Val Pro Ala Thr Ala Asn Ala Asp Pro  
 35 40 45  
 Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr  
 50 55 60  
 Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro  
 65 70 75 80  
 Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala  
 85 90 95  
 Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Val Ile Ala Pro  
 100 105 110  
 Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser  
 115 120 125  
 Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp  
 130 135 140  
 Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro  
 145 150 155 160  
 Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg  
 165 170 175  
 Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala  
 180 185 190  
 Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro  
 195 200 205  
 Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val  
 210 215 220  
 Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys  
 225 230 235 240  
 Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn  
 245 250 255  
 Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly  
 260 265 270  
 Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu  
 275 280 285  
 Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro  
 290 295 300  
 Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr  
 305 310 315 320  
 Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala  
 325 330

## (2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Asp Pro Val Asp Ala Val Ile Asn Thr Thr Xaa Asn Tyr Gly Gln Val

10084820 • 20220

1	5	10	15
Val Ala Ala Leu			
20			

## (2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala Val Glu Ser Gly Met Leu Ala Leu Gly Thr Pro Ala Pro Ser			
1	5	10	15

## (2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala Ala Lys			
1	5	10	15
Glu Gly Arg			

## (2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp Pro Ala Trp Gly Pro			
1	5	10	15

## (2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

205220-ET1848007

Asp Ile Gly Ser Glu Ser Thr Glu Asp Gln Gln Xaa Ala Val  
 1 5 10

## (2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 13 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ala Glu Glu Ser Ile Ser Thr Xaa Glu Xaa Ile Val Pro  
 1 5 10

## (2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Asp Pro Glu Pro Ala Pro Pro Val Pro Thr Ala Ala Ala Ala Pro Pro  
 1 5 10 15  
 Ala

## (2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ala Pro Lys Thr Tyr Xaa Glu Glu Leu Lys Gly Thr Asp Thr Gly  
 1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Gln Thr Ser  
 1 5 10 15

10091814 022502

Leu Leu Asn Asn Leu Ala Asp Pro Asp Val Ser Phe Ala Asp  
                  20                 25                 30

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Thr Gly Ser Leu Asn Gln Thr His Asn Arg Arg Ala Asn Glu Arg Lys  
 1 5 10 15  
 Asn Thr Thr Met Lys Met Val Lys Ser Ile Ala Ala Gly Leu Thr Ala  
 20 25 30  
 Ala Ala Ala Ile Gly Ala Ala Ala Gly Val Thr Ser Ile Met Ala  
 35 40 45  
 Gly Gly Pro Val Val Tyr Gln Met Gln Pro Val Val Phe Gly Ala Pro  
 50 55 60  
 Leu Pro Leu Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln  
 65 70 75 80  
 Leu Thr Ser Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala  
 85 90 95  
 Asn Lys Gly Ser Leu Val Glu Gly Ile Gly Gly Thr Glu Ala Arg  
 100 105 110  
 Ile Ala Asp His Lys Leu Lys Lys Ala Ala Glu His Gly Asp Leu Pro  
 115 120 125  
 Leu Ser Phe Ser Val Thr Asn Ile Gln Pro Ala Ala Gly Ser Ala  
 130 135 140  
 Thr Ala Asp Val Ser Val Ser Gly Pro Lys Leu Ser Ser Pro Val Thr  
 145 150 155 160  
 Gln Asn Val Thr Phe Val Asn Gln Gly Gly Trp Met Leu Ser Arg Ala  
 165 170 175  
 Ser Ala Met Glu Leu Leu Gln Ala Ala Gly Xaa  
 180 185

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Asp	Glu	Val	Thr	Val	Glu	Thr	Thr	Ser	Val	Phe	Arg	Ala	Asp	Phe	Leu
1					5					10				15	
Ser	Glu	Leu	Asp	Ala	Pro	Ala	Gln	Ala	Gly	Thr	Glu	Ser	Ala	Val	Ser
							20			25			30		
Gly	Val	Glu	Gly	Leu	Pro	Pro	Gly	Ser	Ala	Leu	Leu	Val	Val	Lys	Arg
							35			40			45		
Gly	Pro	Asn	Ala	Gly	Ser	Arg	Phe	Leu	Leu	Asp	Gln	Ala	Ile	Thr	Ser

50	55	60														
Ala	Gly	Arg	His	Pro	Asp	Ser	Asp	Ile	Phe	Leu	Asp	Asp	Val	Thr	Val	
65																80
Ser	Arg	Arg	His	Ala	Glu	Phe	Arg	Leu	Glu	Asn	Asn	Glu	Phe	Asn	Val	
															95	
Val	Asp	Val	Gly	Ser	Leu	Asn	Gly	Thr	Tyr	Val	Asn	Arg	Glu	Pro	Val	
															110	
Asp	Ser	Ala	Val	Leu	Ala	Asn	Gly	Asp	Glu	Val	Gln	Ile	Gly	Lys	Leu	
															125	
Arg	Leu	Val	Phe	Leu	Thr	Gly	Pro	Lys	Gln	Gly	Glu	Asp	Asp	Gly	Ser	
															140	
Thr	Gly	Gly	Pro													
															145	

## (2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

1	5	10	15												
Gly	Pro	Asp	Arg	Ser	Ala	Ser	Leu	Ser	Leu	Val	Arg	His	Arg	Arg	Gln
															30
Gln	Arg	Asp	Ala	Leu	Cys	Leu	Ser	Ser	Thr	Gln	Ile	Ser	Arg	Gln	Ser
															45
Asn	Leu	Pro	Pro	Ala	Ala	Gly	Gly	Ala	Ala	Asn	Tyr	Ser	Arg	Arg	Asn
															50
Phe	Asp	Val	Arg	Ile	Lys	Ile	Phe	Met	Leu	Val	Thr	Ala	Val	Val	Leu
															65
Leu	Cys	Cys	Ser	Gly	Val	Ala	Thr	Ala	Ala	Pro	Lys	Thr	Tyr	Cys	Glu
															85
Glu	Leu	Lys	Gly	Thr	Asp	Thr	Gly	Gln	Ala	Cys	Gln	Ile	Gln	Met	Ser
															100
Asp	Pro	Ala	Tyr	Asn	Ile	Asn	Ile	Ser	Leu	Pro	Ser	Tyr	Tyr	Pro	Asp
															115
Gln	Lys	Ser	Leu	Glu	Asn	Tyr	Ile	Ala	Gln	Thr	Arg	Asp	Lys	Phe	Leu
															130
Ser	Ala	Ala	Thr	Ser	Thr	Pro	Arg	Glu	Ala	Pro	Tyr	Glu	Leu	Asn	
															145
Ile	Thr	Ser	Ala	Thr	Tyr	Gln	Ser	Ala	Ile	Pro	Pro	Arg	Gly	Thr	Gln
															165
Ala	Val	Val	Xaa	Val	Tyr	His	Asn	Ala	Gly	Gly	Thr	His	Pro	Thr	
															180
Thr	Thr	Tyr	Lys	Ala	Phe	Asp	Trp	Asp	Gln	Ala	Tyr	Arg	Lys	Pro	Ile
															195
Thr	Tyr	Asp	Thr	Leu	Trp	Gln	Ala	Asp	Thr	Asp	Pro	Leu	Pro	Val	Val
															210
Phe	Pro	Ile	Val	Ala	Arg										225
															230

## (2) INFORMATION FOR SEQ ID NO:66:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Thr	Ala	Ala	Ser	Asp	Asn	Phe	Gln	Leu	Ser	Gln	Gly	Gly	Gln	Gly	Phe
1						5			10		15				
Ala	Ile	Pro	Ile	Gly	Gln	Ala	Met	Ala	Ile	Ala	Gly	Gln	Ile	Arg	Ser
			20						25		30				
Gly	Gly	Gly	Ser	Pro	Thr	Val	His	Ile	Gly	Pro	Thr	Ala	Phe	Leu	Gly
			35					40		45					
Leu	Gly	Val	Val	Asp	Asn	Asn	Gly	Asn	Gly	Ala	Arg	Val	Gln	Arg	Val
			50			55				60					
Val	Gly	Ser	Ala	Pro	Ala	Ala	Ser	Leu	Gly	Ile	Ser	Thr	Gly	Asp	Val
			65			70				75		80			
Ile	Thr	Ala	Val	Asp	Gly	Ala	Pro	Ile	Asn	Ser	Ala	Thr	Ala	Met	Ala
				85					90		95				
Asp	Ala	Leu	Asn	Gly	His	His	Pro	Gly	Asp	Val	Ile	Ser	Val	Asn	Trp
			100				105				110				
Gln	Thr	Lys	Ser	Gly	Gly	Thr	Arg	Thr	Gly	Asn	Val	Thr	Leu	Ala	Glu
			115				120				125				
Gly	Pro	Pro	Ala												
			130												

## (2) INFORMATION FOR SEQ ID NO:67:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Val	Pro	Leu	Arg	Ser	Pro	Ser	Met	Ser	Pro	Ser	Lys	Cys	Leu	Ala	Ala
1							5			10		15			
Ala	Gln	Arg	Asn	Pro	Val	Ile	Arg	Arg	Arg	Arg	Leu	Ser	Asn	Pro	Pro
						20			25		30				
Pro	Arg	Lys	Tyr	Arg	Ser	Met	Pro	Ser	Pro	Ala	Thr	Ala	Ser	Ala	Gly
						35		40			45				
Met	Ala	Arg	Val	Arg	Arg	Ala	Ile	Trp	Arg	Gly	Pro	Ala	Thr	Xaa	
						50		55		60					
Ser	Ala	Gly	Met	Ala	Arg	Val	Arg	Arg	Trp	Xaa	Val	Met	Pro	Xaa	Val
			65			70				75		80			
Ile	Gln	Ser	Thr	Xaa	Ile	Arg	Xaa	Xaa	Gly	Pro	Phe	Asp	Asn	Arg	Gly
						85			90		95				
Ser	Glu	Arg	Lys												
			100												

## (2) INFORMATION FOR SEQ ID NO:68:

100848480001 202502 202502 202502 202502

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met	Thr	Asp	Asp	Ile	Leu	Leu	Ile	Asp	Thr	Asp	Glu	Arg	Val	Arg	Thr
1				5					10					15	
Leu	Thr	Leu	Asn	Arg	Pro	Gln	Ser	Arg	Asn	Ala	Leu	Ser	Ala	Ala	Leu
					20				25				30		
Arg	Asp	Arg	Phe	Phe	Ala	Xaa	Leu	Xaa	Asp	Ala	Glu	Xaa	Asp	Asp	Asp
					35				40			45			
Ile	Asp	Val	Val	Ile	Leu	Thr	Gly	Ala	Asp	Pro	Val	Phe	Cys	Ala	Gly
					50				55			60			
Leu	Asp	Leu	Lys	Val	Ala	Gly	Arg	Ala	Asp	Arg	Ala	Ala	Gly	His	Leu
					65				70			75			80
Thr	Ala	Val	Gly	Gly	His	Asp	Gln	Ala	Gly	Asp	Arg	Arg	Asp	Gln	Arg
					85				90			95			
Arg	Arg	Gly	His	Arg	Arg	Ala	Arg	Thr	Gly	Ala	Val	Leu	Arg	His	Pro
					100				105			110			
Asp	Arg	Leu	Arg	Ala	Arg	Pro	Leu	Arg	Arg	His	Pro	Arg	Pro	Gly	Gly
					115				120			125			
Ala	Ala	Ala	His	Leu	Gly	Thr	Gln	Cys	Val	Leu	Ala	Ala	Lys	Gly	Arg
					130				135			140			
His	Arg	Xaa	Gly	Pro	Val	Asp	Glu	Pro	Asp	Arg	Arg	Leu	Pro	Val	Arg
					145				150			155			160
Asp	Arg	Arg													

## (2) INFORMATION FOR SEQ ID NO:69:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met	Lys	Phe	Val	Asn	His	Ile	Glu	Pro	Val	Ala	Pro	Arg	Arg	Ala	Gly
1						5			10				15		
Gly	Ala	Val	Ala	Glu	Val	Tyr	Ala	Glu	Ala	Arg	Arg	Glu	Phe	Gly	Arg
						20			25			30			
Leu	Pro	Glu	Pro	Leu	Ala	Met	Leu	Ser	Pro	Asp	Glu	Gly	Leu	Leu	Thr
						35			40			45			
Ala	Gly	Trp	Ala	Thr	Leu	Arg	Glu	Thr	Leu	Leu	Val	Gly	Gln	Val	Pro
						50			55			60			
Arg	Gly	Arg	Lys	Glu	Ala	Val	Ala	Ala	Ala	Val	Ala	Ala	Ser	Leu	Arg
						65			70			75			80
Cys	Pro	Trp	Cys	Val	Asp	Ala	His	Thr	Thr	Met	Leu	Tyr	Ala	Ala	Gly
						85			90			95			
Gln	Thr	Asp	Thr	Ala	Ala	Ala	Ile	Leu	Ala	Gly	Thr	Ala	Pro	Ala	Ala
						100			105			110			

Gly Asp Pro Asn Ala Pro Tyr Val Ala Trp Ala Ala Gly Thr Gly Thr  
 115 120 125  
 Pro Ala Gly Pro Pro Ala Pro Phe Gly Pro Asp Val Ala Ala Glu Tyr  
 130 135 140  
 Leu Gly Thr Ala Val Gln Phe His Phe Ile Ala Arg Leu Val Leu Val  
 145 150 155 160  
 Leu Leu Asp Glu Thr Phe Leu Pro Gly Gly Pro Arg Ala Gln Gln Leu  
 165 170 175  
 Met Arg Arg Ala Gly Gly Leu Val Phe Ala Arg Lys Val Arg Ala Glu  
 180 185 190  
 His Arg Pro Gly Arg Ser Thr Arg Arg Leu Glu Pro Arg Thr Leu Pro  
 195 200 205  
 Asp Asp Leu Ala Trp Ala Thr Pro Ser Glu Pro Ile Ala Thr Ala Phe  
 210 215 220  
 Ala Ala Leu Ser His His Leu Asp Thr Ala Pro His Leu Pro Pro Pro  
 225 230 235 240  
 Thr Arg Gln Val Val Arg Arg Val Val Gly Ser Trp His Gly Glu Pro  
 245 250 255  
 Met Pro Met Ser Ser Arg Trp Thr Asn Glu His Thr Ala Glu Leu Pro  
 260 265 270  
 Ala Asp Leu His Ala Pro Thr Arg Leu Ala Leu Leu Thr Gly Leu Ala  
 275 280 285  
 Pro His Gln Val Thr Asp Asp Asp Val Ala Ala Ala Arg Ser Leu Leu  
 290 295 300  
 Asp Thr Asp Ala Ala Leu Val Gly Ala Leu Ala Trp Ala Ala Phe Thr  
 305 310 315 320  
 Ala Ala Arg Arg Ile Gly Thr Trp Ile Gly Ala Ala Ala Glu Gly Gln  
 325 330 335  
 Val Ser Arg Gln Asn Pro Thr Gly  
 340

## (2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Asp Asp Pro Asp Met Pro Gly Thr Val Ala Lys Ala Val Ala Asp Ala  
 1 5 10 15  
 Leu Gly Arg Gly Ile Ala Pro Val Glu Asp Ile Gln Asp Cys Val Glu  
 20 25 30  
 Ala Arg Leu Gly Glu Ala Gly Leu Asp Asp Val Ala Arg Val Tyr Ile  
 35 40 45  
 Ile Tyr Arg Gln Arg Arg Ala Glu Leu Arg Thr Ala Lys Ala Leu Leu  
 50 55 60  
 Gly Val Arg Asp Glu Leu Lys Leu Ser Leu Ala Ala Val Thr Val Leu  
 65 70 75 80  
 Arg Glu Arg Tyr Leu Leu His Asp Glu Gln Gly Arg Pro Ala Glu Ser  
 85 90 95  
 Thr Gly Glu Leu Met Asp Arg Ser Ala Arg Cys Val Ala Ala Glu  
 100 105 110

Asp Gln Tyr Glu Pro Gly Ser Ser Arg Arg Trp Ala Glu Arg Phe Ala  
 115 120 125  
 Thr Leu Leu Arg Asn Leu Glu Phe Leu Pro Asn Ser Pro Thr Leu Met  
 130 135 140  
 Asn Ser Gly Thr Asp Leu Gly Leu Leu Ala Gly Cys Phe Val Leu Pro  
 145 150 155 160  
 Ile Glu Asp Ser Leu Gln Ser Ile Phe Ala Thr Leu Gly Gln Ala Ala  
 165 170 175  
 Glu Leu Gln Arg Ala Gly Gly Gly Thr Gly Tyr Ala Phe Ser His Leu  
 180 185 190  
 Arg Pro Ala Gly Asp Arg Val Ala Ser Thr Gly Gly Thr Ala Ser Gly  
 195 200 205  
 Pro Val Ser Phe Leu Arg Leu Tyr Asp Ser Ala Ala Gly Val Val Ser  
 210 215 220  
 Met Gly Gly Arg Arg Gly Ala Cys Met Ala Val Leu Asp Val Ser  
 225 230 235 240  
 His Pro Asp Ile Cys Asp Phe Val Thr Ala Lys Ala Glu Ser Pro Ser  
 245 250 255  
 Glu Leu Pro His Phe Asn Leu Ser Val Gly Val Thr Asp Ala Phe Leu  
 260 265 270  
 Arg Ala Val Gly Arg Asn Gly Leu His Arg Leu Val Asn Pro Arg Thr  
 275 280 285  
 Gly Lys Ile Val Ala Arg Met Pro Ala Ala Glu Leu Phe Asp Ala Ile  
 290 295 300  
 Cys Lys Ala Ala His Ala Gly Gly Asp Pro Gly Leu Val Phe Leu Asp  
 305 310 315 320  
 Thr Ile Asn Arg Ala Asn Pro Val Pro Gly Arg Gly Arg Ile Glu Ala  
 325 330 335  
 Thr Asn Pro Cys Gly Glu Val Pro Leu Leu Pro Tyr Glu Ser Cys Asn  
 340 345 350  
 Leu Gly Ser Ile Asn Leu Ala Arg Met Leu Ala Asp Gly Arg Val Asp  
 355 360 365  
 Trp Asp Arg Leu Glu Glu Val Ala Gly Val Ala Val Arg Phe Leu Asp  
 370 375 380  
 Asp Val Ile Asp Val Ser Arg Tyr Pro Phe Pro Glu Leu Gly Glu Ala  
 385 390 395 400  
 Ala Arg Ala Thr Arg Lys Ile Gly Leu Gly Val Met Gly Leu Ala Glu  
 405 410 415  
 Leu Leu Ala Ala Leu Gly Ile Pro Tyr Asp Ser Glu Glu Ala Val Arg  
 420 425 430  
 Leu Ala Thr Arg Leu Met Arg Arg Ile Gln Gln Ala Ala His Thr Ala  
 435 440 445  
 Ser Arg Arg Leu Ala Glu Glu Arg Gly Ala Phe Pro Ala Phe Thr Asp  
 450 455 460  
 Ser Arg Phe Ala Arg Ser Gly Pro Arg Arg Asn Ala Gln Val Thr Ser  
 465 470 475 480  
 Val Ala Pro Thr Gly  
 485

## (2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

## (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Gly Val Ile Val Leu Asp Leu Glu Pro Arg Gly Pro Leu Pro Thr Glu  
 1 5 10 15  
 Ile Tyr Trp Arg Arg Arg Gly Leu Ala Leu Gly Ile Ala Val Val Val  
 20 25 30  
 Val Gly Ile Ala Val Ala Ile Val Ile Ala Phe Val Asp Ser Ser Ala  
 35 40 45  
 Gly Ala Lys Pro Val Ser Ala Asp Lys Pro Ala Ser Ala Gln Ser His  
 50 55 60  
 Pro Gly Ser Pro Ala Pro Gln Ala Pro Gln Pro Ala Gly Gln Thr Glu  
 65 70 75 80  
 Gly Asn Ala Ala Ala Ala Pro Pro Gln Gly Gln Asn Pro Glu Thr Pro  
 85 90 95  
 Thr Pro Thr Ala Ala Val Gln Pro Pro Val Leu Lys Gly Gly Asp  
 100 105 110  
 Asp Cys Pro Asp Ser Thr Leu Ala Val Lys Gly Leu Thr Asn Ala Pro  
 115 120 125  
 Gln Tyr Tyr Val Gly Asp Gln Pro Lys Phe Thr Met Val Val Thr Asn  
 130 135 140  
 Ile Gly Leu Val Ser Cys Lys Arg Asp Val Gly Ala Ala Val Leu Ala  
 145 150 155 160  
 Ala Tyr Val Tyr Ser Leu Asp Asn Lys Arg Leu Trp Ser Asn Leu Asp  
 165 170 175  
 Cys Ala Pro Ser Asn Glu Thr Leu Val Lys Thr Phe Ser Pro Gly Glu  
 180 185 190  
 Gln Val Thr Thr Ala Val Thr Trp Thr Gly Met Gly Ser Ala Pro Arg  
 195 200 205  
 Cys Pro Leu Pro Arg Pro Ala Ile Gly Pro Gly Thr Tyr Asn Leu Val  
 210 215 220  
 Val Gln Leu Gly Asn Leu Arg Ser Leu Pro Val Pro Phe Ile Leu Asn  
 225 230 235 240  
 Gln Pro Pro Pro Pro Gly Pro Val Pro Ala Pro Gly Pro Ala Gln  
 245 250 255  
 Ala Pro Pro Pro Glu Ser Pro Ala Gln Gly Gly  
 260 265

## (2) INFORMATION FOR SEQ ID NO:72:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Leu Ile Ser Thr Gly Lys Ala Ser His Ala Ser Leu Gly Val Gln Val  
 1 5 10 15  
 Thr Asn Asp Lys Asp Thr Pro Gly Ala Lys Ile Val Glu Val Val Ala  
 20 25 30  
 Gly Gly Ala Ala Ala Asn Ala Gly Val Pro Lys Gly Val Val Val Thr  
 35 40 45

Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Leu Val Ala Ala  
 50 55 60  
 Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Leu Thr Phe Gln Asp  
 65 70 75 80  
 Pro Ser Gly Gly Ser Arg Thr Val Gln Val Thr Leu Gly Lys Ala Glu  
 85 90 95  
 Gln

## (2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Gly Ala Ala Val Ser Leu Leu Ala Ala Gly Thr Leu Val Leu Thr Ala  
 1 5 10 15  
 Cys Gly Gly Gly Thr Asn Ser Ser Ser Gly Ala Gly Gly Thr Ser  
 20 25 30  
 Gly Ser Val His Cys Gly Gly Lys Lys Glu Leu His Ser Ser Gly Ser  
 35 40 45  
 Thr Ala Gln Glu Asn Ala Met Glu Gln Phe Val Tyr Ala Tyr Val Arg  
 50 55 60  
 Ser Cys Pro Gly Tyr Thr Leu Asp Tyr Asn Ala Asn Gly Ser Gly Ala  
 65 70 75 80  
 Gly Val Thr Gln Phe Leu Asn Asn Glu Thr Asp Phe Ala Gly Ser Asp  
 85 90 95  
 Val Pro Leu Asn Pro Ser Thr Gly Gln Pro Asp Arg Ser Ala Glu Arg  
 100 105 110  
 Cys Gly Ser Pro Ala Trp Asp Leu Pro Thr Val Phe Gly Pro Ile Ala  
 115 120 125  
 Ile Thr Tyr Asn Ile Lys Gly Val Ser Thr Leu Asn Leu Asp Gly Pro  
 130 135 140  
 Thr Thr Ala Lys Ile Phe Asn Gly Thr Ile Thr Val Trp Asn Asp Pro  
 145 150 155 160  
 Gln Ile Gln Ala Leu Asn Ser Gly Thr Asp Leu Pro Pro Thr Pro Ile  
 165 170 175  
 Ser Val Ile Phe Arg Ser Asp Lys Ser Gly Thr Ser Asp Asn Phe Gln  
 180 185 190  
 Lys Tyr Leu Asp Gly Val Ser Asn Gly Ala Trp Gly Lys Gly Ala Ser  
 195 200 205  
 Glu Thr Phe Ser Gly Gly Val Gly Val Gly Ala Ser Gly Asn Asn Gly  
 210 215 220  
 Thr Ser Ala Leu Leu Gln Thr Asp Gly Ser Ile Thr Tyr Asn Glu  
 225 230 235 240  
 Trp Ser Phe Ala Val Gly Lys Gln Leu Asn Met Ala Gln Ile Ile Thr  
 245 250 255  
 Ser Ala Gly Pro Asp Pro Val Ala Ile Thr Thr Glu Ser Val Gly Lys  
 260 265 270  
 Thr Ile Ala Gly Ala Lys Ile Met Gly Gln Gly Asn Asp Leu Val Leu  
 275 280 285  
 Asp Thr Ser Ser Phe Tyr Arg Pro Thr Gln Pro Gly Ser Tyr Pro Ile

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290	295	300
Val Leu Ala Thr Tyr Glu Ile Val Cys Ser Lys Tyr Pro Asp Ala Thr		
305	310	315
Thr Gly Thr Ala Val Arg Ala Phe Met Gln Ala Ala Ile Gly Pro Gly		320
	325	330
Gln Glu Gly Leu Asp Gln Tyr Gly Ser Ile Pro Leu Pro Lys Ser Phe		335
	340	345
Gln Ala Lys Leu Ala Ala Val Asn Ala Ile Ser		350
	355	360

## (2) INFORMATION FOR SEQ ID NO:74:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Gln Ala Ala Ala Gly Arg Ala Val Arg Arg Thr Gly His Ala Glu Asp  
 1                       5                       10                       15  
 Gln Thr His Gln Asp Arg Leu His His Cys Arg Arg Ala Ala Val  
 20                       25                       30  
 Val Val Arg Gln Asp Arg Ala Ser Val Ser Ala Thr Ser Ala Arg Pro  
 35                       40                       45  
 Pro Arg Arg His Pro Ala Gln Gly His Arg Arg Arg Val Ala Pro Ser  
 50                       55                       60  
 Gly Gly Arg Arg Arg Pro His Pro His His Val Gln Pro Asp Asp Arg  
 65                       70                       75                       80  
 Arg Asp Arg Pro Ala Leu Leu Asp Arg Thr Gln Pro Ala Glu His Pro  
 85                       90                       95  
 Asp Pro His Arg Arg Gly Pro Ala Asp Pro Gly Arg Val Arg Gly Arg  
 100                      105                       110  
 Gly Arg Leu Arg Arg Val Asp Asp Gly Arg Leu Gln Pro Asp Arg Asp  
 115                      120                       125  
 Ala Asp His Gly Ala Pro Val Arg Gly Arg Gly Pro His Arg Gly Val  
 130                      135                       140  
 Gln His Arg Gly Gly Pro Val Phe Val Arg Arg Val Pro Gly Val Arg  
 145                      150                       155                       160  
 Cys Ala His Arg Arg Gly His Arg Arg Val Ala Ala Pro Gly Gln Gly  
 165                      170                       175  
 Asp Val Leu Arg Ala Gly Leu Arg Val Glu Arg Leu Arg Pro Val Ala  
 180                      185                       190  
 Ala Val Glu Asn Leu His Arg Gly Ser Gln Arg Ala Asp Gly Arg Val  
 195                      200                       205  
 Phe Arg Pro Ile Arg Arg Gly Ala Arg Leu Pro Ala Arg Arg Ser Arg  
 210                      215                       220  
 Ala Gly Pro Gln Gly Arg Leu His Leu Asp Gly Ala Gly Pro Ser Pro  
 225                      230                       235                       240  
 Leu Pro Ala Arg Ala Gly Gln Gln Pro Ser Ser Ala Gly Arg  
 245                      250                       255  
 Arg Ala Gly Gly Ala Glu Arg Ala Asp Pro Gly Gln Arg Gly Arg His  
 260                      265                       270  
 His Gln Gly His Asp Pro Gly Arg Ala Gln Gly Ala Gln Arg Gly Thr

275	280	285
Ala Gly Val Ala His Ala Ala Gly Pro Arg Arg Ala Ala Val Arg		
290	295	300
Asn Arg Pro Arg Arg		
305		

## (2) INFORMATION FOR SEQ ID NO:75:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Ser Ala Val Trp Cys Leu Asn Gly Phe Thr Gly Arg His Arg His Gly	1	5
	10	15
Arg Cys Arg Val Arg Ala Ser Gly Trp Arg Ser Ser Asn Arg Trp Cys		
20	25	30
Ser Thr Thr Ala Asp Cys Cys Ala Ser Lys Thr Pro Thr Gln Ala Ala		
35	40	45
Ser Pro Leu Glu Arg Arg Phe Thr Cys Cys Ser Pro Ala Val Gly Cys		
50	55	60
Arg Phe Arg Ser Phe Pro Val Arg Arg Leu Ala Leu Gly Ala Arg Thr		
65	70	75
Ser Arg Thr Leu Gly Val Arg Arg Thr Leu Ser Gln Trp Asn Leu Ser		
85	90	95
Pro Arg Ala Gln Pro Ser Cys Ala Val Thr Val Glu Ser His Thr His		
100	105	110
Ala Ser Pro Arg Met Ala Lys Leu Ala Arg Val Val Gly Leu Val Gln		
115	120	125
Glu Glu Gln Pro Ser Asp Met Thr Asn His Pro Arg Tyr Ser Pro Pro		
130	135	140
Pro Gln Gln Pro Gly Thr Pro Gly Tyr Ala Gln Gly Gln Gln Thr		
145	150	155
Tyr Ser Gln Gln Phe Asp Trp Arg Tyr Pro Pro Ser Pro Pro Pro Gln		
165	170	175
Pro Thr Gln Tyr Arg Gln Pro Tyr Glu Ala Leu Gly Gly Thr Arg Pro		
180	185	190
Gly Leu Ile Pro Gly Val Ile Pro Thr Met Thr Pro Pro Pro Gly Met		
195	200	205
Val Arg Gln Arg Pro Arg Ala Gly Met Leu Ala Ile Gly Ala Val Thr		
210	215	220
Ile Ala Val Val Ser Ala Gly Ile Gly Gly Ala Ala Ala Ser Leu Val		
225	230	235
Gly Phe Asn Arg Ala Pro Ala Gly Pro Ser Gly Gly Pro Val Ala Ala		
245	250	255
Ser Ala Ala Pro Ser Ile Pro Ala Ala Asn Met Pro Pro Gly Ser Val		
260	265	270
Glu Gln Val Ala Ala Lys Val Val Pro Ser Val Val Met Leu Glu Thr		
275	280	285
Asp Leu Gly Arg Gln Ser Glu Glu Gly Ser Gly Ile Ile Leu Ser Ala		
290	295	300
Glu Gly Leu Ile Leu Thr Asn Asn His Val Ile Ala Ala Ala Lys		

305	310	315	320
Pro Pro Leu Gly Ser Pro Pro Pro Lys Thr Thr Val Thr Phe Ser Asp			
325	330	335	
Gly Arg Thr Ala Pro Phe Thr Val Val Gly Ala Asp Pro Thr Ser Asp			
340	345	350	
Ile Ala Val Val Arg Val Gln Gly Val Ser Gly Leu Thr Pro Ile Ser			
355	360	365	
Leu Gly Ser Ser Ser Asp Leu Arg Val Gly Gln Pro Val Leu Ala Ile			
370	375	380	
Gly Ser Pro Leu Gly Leu Glu Gly Thr Val Thr Gly Ile Val Ser			
385	390	395	400
Ala Leu Asn Arg Pro Val Ser Thr Thr Gly Glu Ala Gly Asn Gln Asn			
405	410	415	
Thr Val Leu Asp Ala Ile Gln Thr Asp Ala Ala Ile Asn Pro Gly Asn			
420	425	430	
Ser Gly Gly Ala Leu Val Asn Met Asn Ala Gln Leu Val Gly Val Asn			
435	440	445	
Ser Ala Ile Ala Thr Leu Gly Ala Asp Ser Ala Asp Ala Gln Ser Gly			
450	455	460	
Ser Ile Gly Leu Gly Phe Ala Ile Pro Val Asp Gln Ala Lys Arg Ile			
465	470	475	480
Ala Asp Glu Leu Ile Ser Thr Gly Lys Ala Ser His Ala Ser Leu Gly			
485	490	495	
Val Gln Val Thr Asn Asp Lys Asp Thr Pro Gly Ala Lys Ile Val Glu			
500	505	510	
Val Val Ala Gly Gly Ala Ala Ala Asn Ala Gly Val Pro Lys Gly Val			
515	520	525	
Val Val Thr Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Leu			
530	535	540	
Val Ala Ala Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Leu Thr			
545	550	555	560
Phe Gln Asp Pro Ser Gly Gly Ser Arg Thr Val Gln Val Thr Leu Gly			
565	570	575	
Lys Ala Glu Gln			
580			

## (2) INFORMATION FOR SEQ ID NO:76:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met Asn Asp Gly Lys Arg Ala Val Thr Ser Ala Val Leu Val Val Leu			
1	5	10	15
Gly Ala Cys Leu Ala Leu Trp Leu Ser Gly Cys Ser Ser Pro Lys Pro			
20	25	30	
Asp Ala Glu Glu Gln Gly Val Pro Val Ser Pro Thr Ala Ser Asp Pro			
35	40	45	
Ala Leu Leu Ala Glu Ile Arg Gln Ser Leu Asp Ala Thr Lys Gly Leu			
50	55	60	
Thr Ser Val His Val Ala Val Arg Thr Thr Gly Lys Val Asp Ser Leu			

65	70	75	80												
Leu	Gly	Ile	Thr	Ser	Ala	Asp	Val	Asp	Val	Arg	Ala	Asn	Pro	Leu	Ala
65	65	90	95												
Ala	Lys	Gly	Val	Cys	Thr	Tyr	Asn	Asp	Glu	Gln	Gly	Val	Pro	Phe	Arg
100	105	110													
Val	Gln	Gly	Asp	Asn	Ile	Ser	Val	Lys	Leu	Phe	Asp	Asp	Trp	Ser	Asn
115	120	125													
Leu	Gly	Ser	Ile	Ser	Glu	Leu	Ser	Thr	Ser	Arg	Val	Leu	Asp	Pro	Ala
130	135	140													
Ala	Gly	Val	Thr	Gln	Leu	Leu	Ser	Gly	Val	Thr	Asn	Leu	Gln	Ala	Gln
145	150	155	160												
Gly	Thr	Glu	Val	Ile	Asp	Gly	Ile	Ser	Thr	Thr	Lys	Ile	Thr	Gly	Thr
165	170	175													
Ile	Pro	Ala	Ser	Ser	Val	Lys	Met	Leu	Asp	Pro	Gly	Ala	Lys	Ser	Ala
180	185	190													
Arg	Pro	Ala	Thr	Val	Trp	Ile	Ala	Gln	Asp	Gly	Ser	His	His	Leu	Val
195	200	205													
Arg	Ala	Ser	Ile	Asp	Leu	Gly	Ser	Gly	Ser	Ile	Gln	Leu	Thr	Gln	Ser
210	215	220													
Lys	Trp	Asn	Glu	Pro	Val	Asn	Val	Asp							
225	230														

## (2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 66 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Val	Ile	Asp	Ile	Ile	Gly	Thr	Ser	Pro	Thr	Ser	Trp	Glu	Gln	Ala	Ala
1					5	10								15	
Ala	Glu	Ala	Val	Gln	Arg	Ala	Arg	Asp	Ser	Val	Asp	Asp	Ile	Arg	Val
			20			25							30		
Ala	Arg	Val	Ile	Glu	Gln	Asp	Met	Ala	Val	Asp	Ser	Ala	Gly	Lys	Ile
	35			40			45								
Thr	Tyr	Arg	Ile	Lys	Leu	Glu	Val	Ser	Phe	Lys	Met	Arg	Pro	Ala	Gln
	50			55			60								
Pro	Arg														
65															

## (2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 69 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Val	Pro	Pro	Ala	Pro	Pro	Leu	Pro	Pro	Leu	Pro	Pro	Ser	Pro	Ile	Ser
1						5							10		15

Cys Ala Ser Pro Pro Ser Pro Pro Leu Pro Pro Ala Pro Pro Val Ala  
 20 25 30  
 Pro Gly Pro Pro Met Pro Pro Leu Asp Pro Trp Pro Pro Ala Pro Pro  
 35 40 45  
 Leu Pro Tyr Ser Thr Pro Pro Gly Ala Pro Leu Pro Pro Ser Pro Pro  
 50 55 60  
 Ser Pro Pro Leu Pro  
 65

## (2) INFORMATION FOR SEQ ID NO:79:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met Ser Asn Ser Arg Arg Ser Leu Arg Trp Ser Trp Leu Leu Ser  
 1 5 10 15  
 Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala  
 20 25 30  
 Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Pro Ala Leu  
 35 40 45  
 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val  
 50 55 60  
 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr  
 65 70 75 80  
 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val  
 85 90 95  
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln  
 100 105 110  
 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala  
 115 120 125  
 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly  
 130 135 140  
 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly  
 145 150 155 160  
 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu  
 165 170 175  
 Gly Gln Thr Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr  
 180 185 190  
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser  
 195 200 205  
 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr  
 210 215 220  
 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala  
 225 230 235 240  
 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly  
 245 250 255  
 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu  
 260 265 270  
 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val  
 275 280 285

Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile  
 290 295 300  
 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp  
 305 310 315 320  
 Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln  
 325 330 335  
 Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly  
 340 345 350  
 Pro Pro Ala  
 355

## (2) INFORMATION FOR SEQ ID NO:80:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Ser Pro Lys Pro Asp Ala Glu Glu Gln Gly Val Pro Val Ser Pro Thr  
 1 5 10 15  
 Ala Ser Asp Pro Ala Leu Leu Ala Glu Ile Arg Gln Ser Leu Asp Ala  
 20 25 30  
 Thr Lys Gly Leu Thr Ser Val His Val Ala Val Arg Thr Thr Gly Lys  
 35 40 45  
 Val Asp Ser Leu Leu Gly Ile Thr Ser Ala Asp Val Asp Val Arg Ala  
 50 55 60  
 Asn Pro Leu Ala Ala Lys Gly Val Cys Thr Tyr Asn Asp Glu Gln Gly  
 65 70 75 80  
 Val Pro Phe Arg Val Gln Gly Asp Asn Ile Ser Val Lys Leu Phe Asp  
 85 90 95  
 Asp Trp Ser Asn Leu Gly Ser Ile Ser Glu Leu Ser Thr Ser Arg Val  
 100 105 110  
 Leu Asp Pro Ala Ala Gly Val Thr Gln Leu Leu Ser Gly Val Thr Asn  
 115 120 125  
 Leu Gln Ala Gln Gly Thr Glu Val Ile Asp Gly Ile Ser Thr Thr Lys  
 130 135 140  
 Ile Thr Gly Thr Ile Pro Ala Ser Ser Val Lys Met Leu Asp Pro Gly  
 145 150 155 160  
 Ala Lys Ser Ala Arg Pro Ala Thr Val Trp Ile Ala Gln Asp Gly Ser  
 165 170 175  
 His His Leu Val Arg Ala Ser Ile Asp Leu Gly Ser Gly Ser Ile Gln  
 180 185 190  
 Leu Thr Gln Ser Lys Trp Asn Glu Pro Val Asn Val Asp  
 195 200 205

## (2) INFORMATION FOR SEQ ID NO:81:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Gly Asp Ser Phe Trp Ala Ala Ala Asp Gln Met Ala Arg Gly Phe Val  
 1 5 10 15  
 Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln  
 20 25 30  
 His Ala Asp Gly His Ser Leu Leu Leu Asp Ala Thr Asn Pro Ala Val  
 35 40 45  
 Val Ala Tyr Asp Pro Ala Phe Ala Tyr Glu Ile Gly Tyr Ile Xaa Glu  
 50 55 60  
 Ser Gly Leu Ala Arg Met Cys Gly Glu Asn Pro Glu Asn Ile Phe Phe  
 65 70 75 80  
 Tyr Ile Thr Val Tyr Asn Glu Pro Tyr Val Gln Pro Pro Glu Pro Glu  
 85 90 95  
 Asn Phe Asp Pro Glu Gly Val Leu Gly Gly Ile Tyr Arg Tyr His Ala  
 100 105 110  
 Ala Thr Glu Gln Arg Thr Asn Lys Xaa Gln Ile Leu Ala Ser Gly Val  
 115 120 125  
 Ala Met Pro Ala Ala Leu Arg Ala Ala Gln Met Leu Ala Ala Glu Trp  
 130 135 140  
 Asp Val Ala Ala Asp Val Trp Ser Val Thr Ser Trp Gly Glu Leu Asn  
 145 150 155 160  
 Arg Asp Gly Val Val Ile Glu Thr Glu Lys Leu Arg His Pro Asp Arg  
 165 170 175  
 Pro Ala Gly Val Pro Tyr Val Thr Arg Ala Leu Glu Asn Ala Arg Gly  
 180 185 190  
 Pro Val Ile Ala Val Ser Asp Trp Met Arg Ala Val Pro Glu Gln Ile  
 195 200 205  
 Arg Pro Trp Val Pro Gly Thr Tyr Leu Thr Leu Gly Thr Asp Gly Phe  
 210 215 220  
 Gly Phe Ser Asp Thr Arg Pro Ala Gly Arg Arg Tyr Phe Asn Thr Asp  
 225 230 235 240  
 Ala Glu Ser Gln Val Gly Arg Gly Phe Gly Arg Gly Trp Pro Gly Arg  
 245 250 255  
 Arg Val Asn Ile Asp Pro Phe Gly Ala Gly Arg Gly Pro Pro Ala Gln  
 260 265 270  
 Leu Pro Gly Phe Asp Glu Gly Gly Leu Arg Pro Xaa Lys  
 275 280 285

## (2) INFORMATION FOR SEQ ID NO:82:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Thr Lys Phe His Ala Leu Met Gln Glu Gln Ile His Asn Glu Phe Thr  
 1 5 10 15  
 Ala Ala Gln Gln Tyr Val Ala Ile Ala Val Tyr Phe Asp Ser Glu Asp  
 20 25 30  
 Leu Pro Gln Leu Ala Lys His Phe Tyr Ser Gln Ala Val Glu Glu Arg

35	40	45	
Asn His Ala Met Met Leu Val Gln His	Leu Leu Asp Arg Asp	Leu Arg	
50	55	60	
Val Glu Ile Pro Gly Val Asp Thr Val Arg Asn Gln Phe Asp Arg Pro			
65	70	75	80
Arg Glu Ala Leu Ala Ala Leu Asp Gln Glu Arg Thr Val Thr Asp			
85	90	95	
Gln Val Gly Arg Leu Thr Ala Val Ala Arg Asp Glu Gly Asp Phe Leu			
100	105	110	
Gly Glu Gln Phe Met Gln Trp Phe Leu Gln Glu Gln Ile Glu Glu Val			
115	120	125	
Ala Leu Met Ala Thr Leu Val Arg Val Ala Asp Arg Ala Gly Ala Asn			
130	135	140	
Leu Phe Glu Leu Glu Asn Phe Val Ala Arg Glu Val Asp Val Ala Pro			
145	150	155	160
Ala Ala Ser Gly Ala Pro His Ala Ala Gly Gly Arg Leu			
165	170		

## (2) INFORMATION FOR SEQ ID NO:83:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Arg Ala Asp Glu Arg Lys Asn Thr Thr Met Lys Met Val Lys Ser Ile			
1	5	10	15
Ala Ala Gly Leu Thr Ala Ala Ala Ala Ile Gly Ala Ala Ala Ala Gly			
20	25	30	
Val Thr Ser Ile Met Ala Gly Gly Pro Val Val Tyr Gln Met Gln Pro			
35	40	45	
Val Val Phe Gly Ala Pro Leu Pro Leu Asp Pro Xaa Ser Ala Pro Xaa			
50	55	60	
Val Pro Thr Ala Ala Gln Trp Thr Xaa Leu Leu Asn Xaa Leu Xaa Asp			
65	70	75	80
Pro Asn Val Ser Phe Xaa Asn Lys Gly Ser Leu Val Glu Gly Gly Ile			
85	90	95	
Gly Gly Xaa Glu Gly Xaa Xaa Arg Xaa Gln			
100	105		

## (2) INFORMATION FOR SEQ ID NO:84:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Val Leu Ser Val Pro Val Gly Asp Gly Phe Trp Xaa Arg Val Val Asn			
1	5	10	15
Pro Leu Gly Gln Pro Ile Asp Gly Arg Gly Asp Val Asp Ser Asp Thr			

20	25	30	
Arg Arg Ala Leu Glu Leu Gln Ala Pro Ser Val Val Xaa Arg Gln Gly			
35	40	45	
Val Lys Glu Pro Leu Xaa Thr Gly Ile Lys Ala Ile Asp Ala Met Thr			
50	55	60	
Pro Ile Gly Arg Gly Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr			
65	70	75	80
Gly Lys Asn Arg Arg Leu Cys Arg Thr Pro Ser Ser Asn Gln Arg Glu			
85	90	95	
Glu Leu Gly Val Arg Trp Ile Pro Arg Ser Arg Cys Ala Cys Val Tyr			
100	105	110	
Val Gly His Arg Ala Arg Arg Gly Thr Tyr His Arg Arg			
115	120	125	

## (2) INFORMATION FOR SEQ ID NO:85:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Cys Asp Ala Val Met Gly Phe Leu Gly Gly Ala Gly Pro Leu Ala Val			
1	5	10	15
Val Asp Gln Gln Leu Val Thr Arg Val Pro Gln Gly Trp Ser Phe Ala			
20	25	30	
Gln Ala Ala Ala Val Pro Val Val Phe Leu Thr Ala Trp Tyr Gly Leu			
35	40	45	
Ala Asp Leu Ala Glu Ile Lys Ala Gly Glu Ser Val Leu Ile His Ala			
50	55	60	
Gly Thr Gly Gly Val Gly Met Ala Ala Val Gln Leu Ala Arg Gln Trp			
65	70	75	80
Gly Val Glu Val Phe Val Thr Ala Ser Arg Gly Lys Trp Asp Thr Leu			
85	90	95	
Arg Ala Xaa Xaa Phe Asp Asp Xaa Pro Tyr Arg Xaa Phe Pro His Xaa			
100	105	110	
Arg Ser Ser Xaa Gly			
115			

## (2) INFORMATION FOR SEQ ID NO:86:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met Tyr Arg Phe Ala Cys Arg Thr Leu Met Leu Ala Ala Cys Ile Leu			
1	5	10	15
Ala Thr Gly Val Ala Gly Leu Gly Val Gly Ala Gln Ser Ala Ala Gln			
20	25	30	

Thr Ala Pro Val Pro Asp Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp  
 35 40 45  
 Pro Ala Trp Gly Pro Asn Trp Asp Pro Tyr Thr Cys His Asp Asp Phe  
 50 55 60  
 His Arg Asp Ser Asp Gly Pro Asp His Ser Arg Asp Tyr Pro Gly Pro  
 65 70 75 80  
 Ile Leu Glu Gly Pro Val Leu Asp Asp Pro Gly Ala Ala Pro Pro Pro  
 85 90 95  
 Pro Ala Ala Gly Gly Gly Ala  
 100

## (2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Val Gln Cys Arg Val Trp Leu Glu Ile Gln Trp Arg Gly Met Leu Gly  
 1 5 10 15  
 Ala Asp Gln Ala Arg Ala Gly Gly Pro Ala Arg Ile Trp Arg Glu His  
 20 25 30  
 Ser Met Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala  
 35 40 45  
 Thr Lys Glu Gly Arg Gly Ile Val Met Arg Val Pro Leu Glu Gly Gly  
 50 55 60  
 Gly Arg Leu Val Val Glu Leu Thr Pro Asp Glu Ala Ala Ala Leu Gly  
 65 70 75 80  
 Asp Glu Leu Lys Gly Val Thr Ser  
 85

## (2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile  
 1 5 10 15  
 Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly  
 20 25 30  
 Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala  
 35 40 45  
 Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu  
 50 55 60  
 Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg  
 65 70 75 80  
 Ala Asp Glu Glu Gln Gln Ala Leu Ser Ser Gln Met Gly Phe

100844843 022502

85

90

95

## (2) INFORMATION FOR SEQ ID NO:89:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Met	Thr	Gln	Ser	Gln	Thr	Val	Thr	Val	Asp	Gln	Gln	Glu	Ile	Leu	Asn
1															
															15
Arg	Ala	Asn	Glu	Val	Glu	Ala	Pro	Met	Ala	Asp	Pro	Pro	Thr	Asp	Val
20															
															30
Pro	Ile	Thr	Pro	Cys	Glu	Leu	Thr	Xaa	Xaa	Lys	Asn	Ala	Ala	Gln	Gln
35															
															45
Xaa	Val	Leu	Ser	Ala	Asp	Asn	Met	Arg	Glu	Tyr	Leu	Ala	Ala	Gly	Ala
50															
															60
Lys	Glu	Arg	Gln	Arg	Leu	Ala	Thr	Ser	Leu	Arg	Asn	Ala	Ala	Lys	Xaa
65															
															80
Tyr	Gly	Glu	Val	Asp	Glu	Ala	Ala	Thr	Ala	Leu	Asp	Asn	Asp	Gly	
85															95
Glu	Gly	Thr	Val	Gln	Ala	Glu	Ser	Ala	Gly	Ala	Val	Gly	Gly	Asp	Ser
100															110
Ser	Ala	Glu	Leu	Thr	Asp	Thr	Pro	Arg	Val	Ala	Thr	Ala	Gly	Glu	Pro
115															125
Asn	Phe	Met	Asp	Leu	Lys	Glu	Ala	Ala	Arg	Lys	Leu	Glu	Thr	Gly	Asp
130															
															140
Gln	Gly	Ala	Ser	Leu	Ala	His	Xaa	Gly	Asp	Gly	Trp	Asn	Thr	Xaa	Thr
145															160
Leu	Thr	Leu	Gln	Gly	Asp										
															165

## (2) INFORMATION FOR SEQ ID NO:90:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Arg	Ala	Glu	Arg	Met
1				5

## (2) INFORMATION FOR SEQ ID NO:91:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala Ala  
 1 5 10 15  
 Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr  
 20 25 30  
 Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu  
 35 40 45  
 Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val Asn  
 50 55 60  
 Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met Phe  
 65 70 75 80  
 Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe  
 85 90 95  
 Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln Ala  
 100 105 110  
 Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Asn Gln Leu Met  
 115 120 125  
 Asn Asn Val Pro Gln Ala Leu Lys Gln Leu Ala Gln Pro Thr Gln Gly  
 130 135 140  
 Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser Pro  
 145 150 155 160  
 His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His Met  
 165 170 175  
 Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser Met  
 180 185 190  
 Leu Lys Gly Phe Ala Pro Ala Ala Ala Gln Ala Val Gln Thr Ala  
 195 200 205  
 Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly  
 210 215 220  
 Ser Ser Gly Leu Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala  
 225 230 235 240  
 Ser Val Arg Tyr Gly His Arg Asp Gly Gly Lys Tyr Ala Xaa Ser Gly  
 245 250 255  
 Arg Arg Asn Gly Gly Pro Ala  
 260

## (2) INFORMATION FOR SEQ ID NO:92:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Met Thr Tyr Ser Pro Gly Asn Pro Gly Tyr Pro Gln Ala Gln Pro Ala  
 1 5 10 15  
 Gly Ser Tyr Gly Gly Val Thr Pro Ser Phe Ala His Ala Asp Glu Gly  
 20 25 30  
 Ala Ser Lys Leu Pro Met Tyr Leu Asn Ile Ala Val Ala Val Leu Gly  
 35 40 45  
 Leu Ala Ala Tyr Phe Ala Ser Phe Gly Pro Met Phe Thr Leu Ser Thr

50	55	60	
Glu Leu Gly Gly Gly Asp Gly Ala Val Ser Gly Asp Thr Gly Leu Pro			
65	70	75	80
Val Gly Val Ala Leu Leu Ala Ala Leu Leu Ala Gly Val Val Leu Val			
85	90	95	
Pro Lys Ala Lys Ser His Val Thr Val Val Ala Val Leu Gly Val Leu			
100	105	110	
Gly Val Phe Leu Met Val Ser Ala Thr Phe Asn Lys Pro Ser Ala Tyr			
115	120	125	
Ser Thr Gly Trp Ala Leu Trp Val Val Leu Ala Phe Ile Val Phe Gln			
130	135	140	
Ala Val Ala Ala Val Leu Ala Leu Leu Val Glu Thr Gly Ala Ile Thr			
145	150	155	160
Ala Pro Ala Pro Arg Pro Lys Phe Asp Pro Tyr Gly Gln Tyr Gly Arg			
165	170	175	
Tyr Gly Gln Tyr Gly Gln Tyr Gly Val Gln Pro Gly Gly Tyr' Tyr Gly			
180	185	190	
Gln Gln Gly Ala Gln Gln Ala Ala Gly Leu Gln Ser Pro Gly Pro Gln			
195	200	205	
Gln Ser Pro Gln Pro Pro Gly Tyr Gly Ser Gln Tyr Gly Gly Tyr Ser			
210	215	220	
Ser Ser Pro Ser Gln Ser Gly Ser Gly Tyr Thr Ala Gln Pro Pro Ala			
225	230	235	240
Gln Pro Pro Ala Gln Ser Gly Ser Gln Gln Ser His Gln Gly Pro Ser			
245	250	255	
Thr Pro Pro Thr Gly Phe Pro Ser Phe Ser Pro Pro Pro Pro Val Ser			
260	265	270	
Ala Gly Thr Gly Ser Gln Ala Gly Ser Ala Pro Val Asn Tyr Ser Asn			
275	280	285	
Pro Ser Gly Gly Glu Gln Ser Ser Ser Pro Gly Gly Ala Pro Val			
290	295	300	

## (2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Gly Cys Gly Glu Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn			
1	5	10	15
Phe Glu Arg Ile Ser Gly Asp Leu Lys Thr Gln Ile			
20	25		

## (2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly  
1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:95:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Gly Cys Gly Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala  
1 5 10 15  
Ala Gly Thr Ala Ala Gln Ala Ala Val Val Arg  
20 25

## (2) INFORMATION FOR SEQ ID NO:96:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Gly Cys Gly Gly Thr Ala Ala Gln Ala Ala Val Val Arg Phe Gln Glu  
1 5 10 15  
Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu  
20 25

## (2) INFORMATION FOR SEQ ID NO:97:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Gly Cys Gly Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile Ser Thr  
1 5 10 15  
Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg  
20 25

## (2) INFORMATION FOR SEQ ID NO:98:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Gly	Cys	Gly	Ile	Arg	Gln	Ala	Gly	Val	Gln	Tyr	Ser	Arg	Ala	Asp	Glu	
1																
														15		
Glu		Gln		Gln		Ala		Leu		Ser		Gln		Met	Gly	Phe
														20		
															25	

## (2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 507 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

ATGAAAGATGG	TGAAATCGAT	CGCCGCAGGT	CTGACCGCCG	CGGCTGCAAT	CGGC CGCGCT	60
GCGCCCGGTG	TGACTTCGAT	CATGGCTGGC	GCCCCGGTCG	TATACCAAGAT	GCAGCCCGTC	120
GTCTTCGGCG	CGCCACTGCG	GTGGACCGG	GCATCGGCC	CTGACGTTCC	GACCGCCGCC	180
CAGTTGACCA	CGCCCTCGCC	GATCCAACG	TGTCGTTTC	GAACAAGGGC	240	
AGTCTGGTCG	AGGGCGGCAT	CGGGGCACCC	GGGGCGCGCA	TGGCCGACCA	CAAGCTGAAG	300
AAGGCCCGCG	AGCACGGGGA	TCTGCGCTG	TGTTCAAGCG	TGACGAACAT	CCAGCCCGCG	360
GCCGCCGGTT	CGGCCAACCG	CGACGTTTC	GTCTCGGGTC	CGAACGCTTC	GTCGCCGGTC	420
ACGAGAACG	TCACGTTCGT	GAATCAAGGC	GGCTGGATGC	TGTACCGGCC	ATCGGCCGATG	480
GAGTTGTCG	AGGCCGCAAG	GAAGTGA				507

## (2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 168 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Met	Lys	Met	Val	Lys	Ser	Ile	Ala	Ala	Gly	Leu	Thr	Ala	Ala	Ala	Ala
1															
														15	
Ile	Gly	Ala	Ala	Ala	Ala	Gly	Val	Thr	Ser	Ile	Met	Ala	Gly	Gly	Pro
														30	
Val	Val	Tyr	Gln	Met	Gln	Pro	Val	Val	Phe	Gly	Ala	Pro	Leu	Pro	Leu
														45	
Asp	Pro	Ala	Ser	Ala	Pro	Asp	Val	Pro	Thr	Ala	Ala	Gln	Leu	Thr	Ser
														50	
Leu	Leu	Asn	Ser	Leu	Ala	Asp	Pro	Asn	Val	Ser	Phe	Ala	Asn	Lys	Gly
														60	
Ser	Leu	Val	Glu	Gly	Ile	Gly	Gly	Thr	Glu	Ala	Arg	Ile	Ala	Asp	
														85	
His	Lys	Leu	Lys	Lys	Ala	Ala	Glu	His	Gly	Asp	Leu	Pro	Leu	Ser	Phe

100	105	110
Ser Val Thr Asn Ile Gln Pro Ala Ala Ala Gly Ser Ala Thr Ala Asp		
115	120	125
Val Ser Val Ser Gly Pro Lys Leu Ser Ser Pro Val Thr Gln Asn Val		
130	135	140
Thr Phe Val Asn Gln Gly Gly Trp Met Leu Ser Arg Ala Ser Ala Met		
145	150	155
Glu Leu Leu Gln Ala Ala Gly Asn		
165		

## (2) INFORMATION FOR SEQ ID NO:101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

CTGGCCAATG TCGTTGACCG TCGGGGCGCG GGTCGCCCTCC GCAGATCCCC	60
CATTAAACACC ACCTTCAATT ACGGGCAGGT AGTAGCTGGC CTCAACCGGA CGGATCCGGG	120
GGCTGCCGCA CAGTTCAACG CCTCACCGGT GGGCGAGTCC TATTTGCGCA ATTTCCTCGC	180
CGCACCGCCA CCTTCAGCGG CCTGCCATGGC CGCGCAATGG CAAGCTGGC CGGGGGCGGC	240
ACAGTACATC GGCCTTGTGC AGTCGGTTGC CGGCTCTTGC AACAATTATT AAGCCCCATGC	300
GGGGCCCCATC CCGCGACCCG GCATCGTGC CGGGGCTAGG CCAGATTGCC CCGCTCTCA	360
ACGGGGCGCA TCCCGGACCC CGGCATCTGC GCCGGGGCTA GGCCAGATGTG CCCCGCTCT	420
CAACGGGGCCG CATCTGTGC CGAATTCTGT CAGCCCCGGG GATCCACTAG TTCTAGAGCG	480
GCCGCCACCG CGGTGGAGCT	500

## (2) INFORMATION FOR SEQ ID NO:102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Val Ala Met Ser Leu Thr Val Gly Ala Gly Val Ala Ser Ala Asp Pro	
1 5 10 15	
Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val Val Ala	
20 25 30	
Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser	
35 40 45	
Pro Val Ala Gln Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro	
50 55 60	
Gln Arg Ala Ala Met Ala Ala Gln Leu Gln Ala Val Pro Gly Ala Ala	
65 70 75 80	
Gln Tyr Ile Gly Leu Val Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr	
85 90 95	

## (2) INFORMATION FOR SEQ ID NO:103:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

ATGACAGAGC AGCAGTGGAA TTTGGCGGTG ATCGAGGGCG CGGCAAGCGC AATCCAGGGA	60
ATATGTCAGCT CCATTCACTT CCTCTTGTAC GAGGGGAAGC AGTCCCTGAC CAAGCTCGCA	120
GCAGGCTCTGGG GCGGTAGCGG TTTCGGAAGCGC TACC	154

## (2) INFORMATION FOR SEQ ID NO:104:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met Thr Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala Ser	
1 5 10 15	
Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly	
20 25 30	
Lys Gln Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly Ser	
35 40 45	
Glu Ala Tyr	
50	

## (2) INFORMATION FOR SEQ ID NO:105:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CGGTGCGCA CTTCCAGGTG ACTATGAAAG TCGGCTTCGG NCTGGAGGAT TCCTGAACCT	60
TCAAGGGCGG CCGATAACTG AGGTGCACTCA TTAAGCGACT TTTCAGAAC ATCTGACGC	120
GCTCGAAACG CGGCACAGCG GACGGTGGCT CCGNCAGGC GCTGNCTCCA AAATCCCTGA	180
GACAATTCGN CGGGGGCGCC TACAAAGGAAG TCGGTGCTGA ATTGCGNCNG TATCTGGTCG	240
ACCTGTGTGG TCTGNAGCGG GACGAAGCGG TGCTCGACGT CG	282

## (2) INFORMATION FOR SEQ ID NO:106:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GATCGTACCC	GTGCGAGTGC	TGGGGCCGTT	TGAGGATGGA	GTGACACGTTG	CTTTCGTGAT	60
GGCATACCCA	GAGATGTTGG	CGGCGGCGGC	TGACACCCCTG	CAGAGCATCG	GTGCTACCAC	120
TGTGGCTAGC	AATGCGCTG	CGGCGGCCCC	GACGACTGGG	GTGGTGCCTCC	CCGCTGCCGA	180
TGAGGTTGTCG	GCGCTGACTG	CGGGCGACTT	CGCCGCACAT	CGGGCGATGT	ATCAGTCCGT	240
GAGCGCTCGG	GCTGCTGCGA	TTCATGACCA	GTTCGTGCCC	ACCCCTGCCA	GCAGCGCCAG	300
CTCGTATGCG	GCCACTGAAG	TGCGCAATGC	GGCGCGGCC	AGCTAAGCCA	GGAACAGTCG	360
GCACGAGAAA	CCACGAGAAA	TAGGGACACG	TAATGGTGG	TTTCGGGGCG	TTACCAACGG	420
AGATCAACTC	CGCGAGGATG	TACGCGGCC	CGGGTTCGGC	CTCGCTGGTG	GCCCGCGCTC	480
AGATGTGGGA	CAGCGTGGCG	AGTGACCTGT	TTTCGGCCGC	GTGCGCGTTT	CAGTCGGTGG	540
TCTGGGGTCT	GACGGTGGGG	TCGTGGATAG	GTTCGTCCGC	GGGTCTGATG	GTGGCGCCGG	600
CCTCGCCGTA	TGTGGCGTGG	ATGAGCGTCA	CCGCGGGGCA	GGCCGAGCTG	ACCGCCGCC	660
AGGTCCGGGT	TGCTGCGGCC	GCCTACGAGA	CGGCGTATGG	GCTGACGGTG	CCCCCGCCGG	720
TGATCGCCGA	GAACCGTGT	GAACGTGATGA	TTCTGATAGC	GACCAACCTC	TTGGGGAAA	780
ACACCCCGC	GATCGCGTC	AACGAGGCCG	AATACGGCGA	GATGTGGGCC	CAAGACGCCG	840
CCCGCGATGTT	TGGCTACGCC	CGGGCGACGG	CGACGGCGAC	GGGCACGTTG	CTGCCGTTCG	900
AGGAGGGGCC	GGAGATGACC	AACGGCGGTG	GGCTCTCGA	GCAGGCC	GGCGTCCAGG	960
AGGCCTCCGA	CACCGCCGCG	GCGAACCGT	TGATGACAA	TGTGCCCCAG	GCGCTGCAAC	1020
AGCTGGGCCA	GCCCACCGAG	GGCACCCACG	CTTCTTCAA	GCTGGGGTGC	CTGTTGAAGA	1080
CGGTCTCGCC	GCATCGGTG	CGGATCAGCA	ACATGGTGT	GATGGCCAC	AACCACTGTT	1140
CGATGACCAA	CTCGGGTGTG	TGATGACCA	ACACCTTGAG	CTCGATGTTG	AAGGGCTTGT	1200
CTCCGGCGGC	GGCCGCCAG	GGCGTCAA	CCGCGGCCA	AAACGGGTC	CGGGCGATGA	1260
GCTCGCTGGG	CACTCGCTG	GGTCTTCCG	GTCTGGCGG	TGGGTGGCC	GCCAACTTGG	1320
GTCGGGCGGC	CTCGGTCGGT	TGATGACCA	ACACCTTGAG	CTCGATGTTG	AAGGGCTTGT	1380
CAGTCACCCC	GGCGCGCCGG	GGCGTCCGC	TGACCAAGCT	GACCGAGGCC	GCGGAAAGAG	1440
GGCCCGGGCA	GATGCTGGG	GGGCTGCCG	TGGGGAGAT	GGGC	GGCAGGCCAG	1500
GGCTCAGTGG	TGTGCTGCGT	GTTCGCGCCG	GACCTATGT	GATGCCGAT	TCTCCGGCGG	1560
CGGGCTAGGA	GAGGGGGCGC	AGACTGTCGT	TATTTGACCA	GTGATCGCG	GTCTCGGTGT	1620

GGCTATGACA	ACAGCTAATG	TGCTATGACAA	TTTACAGGTA	TTAGGTCAG	1680
GTTCAACAAG	GAGACAGGCA	ACATGGCCTC	ACGTTTTATG	ACGGATCCGC	1740
GGGACATGGCG	GGCGGTTTG	AGGTGCAACG	CCAGACGGTG	GGGGACGAGG	1800
GTGGGCGTCC	GCGAAACAA	TTTCGGTGC	GGGCTGGAGT	GGCATGGCG	1860
GCTAGACACC	ATGGCCCAGA	TGAATCAGGC	GTTCGCAAC	ATCGTAAACA	1920
GGTGCCTGAC	GGGCTGGTT	GCGACGCCAA	CAACTACGAG	CAGCAAGAGC	1980
GCAGATCCCTC	AGCAGCTAAC	GTCAGCCGCT	GCAGCACAA	ACTTTTACAA	2040
ACAGGTTCGA	TGACCATCAA	CTATCAATT	GGGGATGTCG	ACGCTCACGG	2100
CGCGCTCAGG	CGGGGTTGCT	GGAGGCCGAG	CATCAGGCCA	TCATTCGTA	2160
GCGAGTGTACT	TTTGGGGCGG	CGCGGTTGCG	CGGGCCTGCC	AGGGGTTCAT	2220
GGCCGTAACT	TCCAGGTGAT	CTACGAGCAG	GCCAAACGCC	ACGGGCAGAA	2280
GCCGGCAACA	ACATGGCGCA	AACCGACAGC	CGCGTCGGCT	CGAGCTGGC	2340
GCCAAGGCCA	GGGACGTGGT	GTACGAGTGA	AGTTCTCTGC	GTGATCCCTC	2400
CTAAGTGGTC	AGTGTCTGGG	TGTTGGTGGT	TTGCTGCTTG	CGGGGTTCTT	2460
CAGTGTCTGCT	CGGGCTCGGG	TGAGGACCTC	GAGGCCAGG	TAGGCCGTC	2520
TTCTCGTGT	TGTTCGCGA	GGACGGCTCC	GACGAGGCGG	ATGATCGAGG	2580
GAAGATGCC	ACGACGTCCG	TTCCGGCTCG	TACCTCTCGG	TTGAGGCGTT	2640
GTTGGACCA	ATTTGGGCC	AGATCTGCTT	GGGGAGGCC	GTGAAACGCCA	2700
CGGGGCGGTG	TCGAGGTGCT	CGGCCACCGC	GGGGAGTTG	TCGGTCAGAG	2760
CCGATCATAT	TGGCAACAA	CTGATTCTGGC	GTCCGGCTCG	TCGTAGATGG	2820
GGTGCGCACC	CACGGCCAGG	AGGGCTTCGG	GGTGGCTGCC	ATCAGATGG	2880
GGTTCTGCAG	CGCTGCCAGG	CCGCTGCCGG	CAGGGTGGCG	CCGATGCCGG	2940
GGCGTGGGCG	TCGCTGGTGA	CCAGCGCAGC	CCCGGACAGG	CCGGGGGCCA	3000
GGAGAACGCC	AGCCAGCCGG	CCCCGGCTCTC	GGGGGAGGTG	ACCTGGATGC	3058

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

## (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Met Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met  
 1 5 10 15  
 Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp  
 20 25 30  
 Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser  
 35 40 45  
 Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly  
 50 55 60  
 Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr  
 65 70 75 80  
 Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala  
 85 90 95  
 Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala  
 100 105 110  
 Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly  
 115 120 125  
 Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met  
 130 135 140  
 Trp Ala Gln Asp Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala  
 145 150 155 160  
 Thr Ala Thr Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr  
 165 170 175  
 Ser Ala Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser  
 180 185 190  
 Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu  
 195 200 205  
 Gln Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu  
 210 215 220  
 Gly Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn  
 225 230 235 240  
 Met Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val  
 245 250 255  
 Ser Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala  
 260 265 270

Ala Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala  
 275 280 285  
 Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly  
 290 295 300  
 Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val  
 305 310 315 320  
 Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg  
 325 330 335  
 Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly  
 340 345 350  
 Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly  
 355 360 365  
 Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met  
 370 375 380  
 Pro His Ser Pro Ala Ala Gly  
 385 390

## (2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1725 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GACGTCAGCA CCCGCCGTGC	AGGGCTGGAG CGTGGCTGGT	TTTGATCTGC	GGTCAAGGTG	60
ACGTCCCTCG	GCGTGTGCC	GGCGTGGATG	CAGACTCGAT	120
ATTCGTTGTA	AGTGCTCGG	AGGTATAAGGA	CTTCACGATT	180
CGTGTGGGG	TCGATTTGGC	CGGACCAGTC	GTCACCAACG	240
GGCGATCAGA	TCGCTTGACT	ACCAATCAAT	CTTGAGCTCC	300
ATGAGGAGGA	GCACCGCTGT	CTTTCACTGC	GCAACCCGAG	360
CGAACTCTCGT	TCCCTGGGGG	CAACGCTGAA	GGCTAGCAAT	420
GACTGGGGTG	GTGCCCCCGG	CTGCCGACGA	GGTGTGCGCTG	480
TACGCGATGCG	CGGACGATAC	AGACGGGCG	GCGCAAGGCC	540
TGTGACCAACG	CTGGCCACCA	GCGCTAGTTG	ATATGCGGAC	600
GGTCACCGGC	TAGCTGACCT	GACGGTATTC	GAGCGGAAGG	660

CGGGGCGTTA	CCACCGGAGA	TCAACTCCGC	GAGGATGTAC	GCCGGCCCG	GTTCGGCCTC	720
GCTGGTGGCC	GCCGCGAAGA	TGTGGGACAG	CGTGGCGAGT	GACCTGTTT	CGGCCGCGTC	780
GGCGTTTCAG	TCGGTGGTCT	GGGGTCTGAC	GGTGGGTCG	TGGATAGGT	CGTCGGCGGG	840
TCTGATGGCG	CGGGCGGCC	CGCCGTATGT	GGCGTGGATG	AGCGTCACCG	CGGGGCAGGC	900
CCAGCTGACC	CCCGCCCAAGG	TCCGGGTTGC	TGCGCGGCC	TACGAGACAG	CGTATAGGCT	960
GACGGTGCCC	CCGCCGGTGA	TGCCGAGAA	CCGTACCGAA	CTGATGACGC	TGACCGCGAC	1020
CAACCTCTT	GGGCAAACAA	CGCCGGCGAT	CGAGGCCAAT	CAGGCCGCAT	ACAGCCAGAT	1080
GTGGGGCCAA	GACGCGGAGG	CGATGTATGG	CTACGCCGC	ACGGCGGCCA	CGGCGACCGA	1140
GGCGTTGCTG	CGGTTGAGG	ACGCCCCACT	GATCACCAAC	CCCGCGGGC	TCTTGAGCA	1200
GGCCGTCGCG	CTCGAGGAGG	CCATCGACAC	CGCCGCGGCC	AACCAGTTGA	TGAACAAATGT	1260
GCCCCAAGCG	CTGCAACAGC	TGGCCCAGCC	AGCGCAGGGC	GTCGTACCTT	CTTCCAAGCT	1320
GGGTGGGCTG	TGGACGGCGG	TCTCGCCGA	TCTGTCGCCG	CTCAGCAACG	TCAGTTGAT	1380
AGCCAACAAAC	CACATGTCGA	TGATGGGCAC	GGGTGTGTCG	ATGACCAACA	CCTTGCACTC	1440
GATGTTGAAG	GGCTTAGCTC	CGCGGGCGGC	TCAGGCCGTG	AAACCCCGG	CGAAACACGG	1500
GGTCTGGGCG	ATGAGCTCGC	TGGCAGCCA	GCTGGGTTCG	TCGCTGGGTT	CTTCGGGTCT	1560
GGCGCGCTGGG	GTGGCCGCCA	ACTTGGGTCG	GGCGGCCCTCG	GTCGGTTCTG	TGTCGGTGCC	1620
GCCAGCATGG	GCCCGCGCCA	ACCAGCGGT	CACCCCGCGC	GCGCGGGCGC	TGCCGCTGAC	1680
CAGCCTGACC	AGCGCCGCC	AAACCGCCCC	CGGACACATG	CTGGG		1725

## (2) INFORMATION FOR SEQ ID NO:109:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Val	Val	Asp	Phe	Gly	Ala	Leu	Pro	Pro	Glu	Ile	Asn	Ser	Ala	Arg	Met
1															

Tyr	Ala	Gly	Pro	Gly	Ser	Ala	Ser	Leu	Val	Ala	Ala	Ala	Lys	Met	Trp

Asp	Ser	Val	Ala	Ser	Asp	Leu	Phe	Ser	Ala	Ala	Ser	Ala	Phe	Gln	Ser

35

40

45

Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly  
 50 55 60

Leu Met Ala Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr  
 65 70 75 80

Ala Gly Gln Ala Gln Leu Thr Ala Ala Gln Val Arg Val Ala Ala  
 85 90 95

Ala Tyr Glu Thr Ala Tyr Arg Leu Thr Val Pro Pro Pro Val Ile Ala  
 100 105 110

Glu Asn Arg Thr Glu Leu Met Thr Leu Thr Ala Thr Asn Leu Leu Gly  
 115 120 125

Gln Asn Thr Pro Ala Ile Glu Ala Asn Gln Ala Ala Tyr Ser Gln Met  
 130 135 140

Trp Gly Gln Asp Ala Glu Ala Met Tyr Gly Tyr Ala Ala Thr Ala Ala  
 145 150 155 160

Thr Ala Thr Glu Ala Leu Leu Pro Phe Glu Asp Ala Pro Leu Ile Thr  
 165 170 175

Asn Pro Gly Gly Leu Leu Glu Gln Ala Val Ala Val Glu Glu Ala Ile  
 180 185 190

Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu  
 195 200 205

Gln Gln Leu Ala Gln Pro Ala Gln Gly Val Val Pro Ser Ser Lys Leu  
 210 215 220

Gly Gly Leu Trp Thr Ala Val Ser Pro His Leu Ser Pro Leu Ser Asn  
 225 230 235 240

Val Ser Ser Ile Ala Asn Asn His Met Ser Met Met Gly Thr Gly Val  
 245 250 255

Ser Met Thr Asn Thr Leu His Ser Met Leu Lys Gly Leu Ala Pro Ala  
 260 265 270

Ala Ala Gln Ala Val Glu Thr Ala Ala Glu Asn Gly Val Trp Ala Met  
 275 280 285

Ser Ser Leu Gly Ser Gln Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu  
 290 295 300

Gly Ala Gly Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser  
 305 310 315 320

Leu Ser Val Pro Pro Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro  
 325 330 335

Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Gln Thr  
 340 345 350 355

Ala Pro Gly His Met Leu Gly  
 355

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3027 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

AGTTCACTGC	AGAATGATAC	TGACGGCTG	TATCCACGAT	GGCTGAGACA	ACCGAACAC	60
CGTCGGACGC	GGGGACATCG	CAAGCCGACG	CGATGGCGTT	GGCCGCCGAA	GCCGAAGCCG	120
CCGAAGCCGA	AGCGCTGGCC	GCCGGGGCCG	GGGCCCCGTC	CCGTGCGGCC	CGGTTGAAGC	180
GTGAGCGCT	GGCGATGGCC	CCAGCCGAGG	ACGAGAACGT	CCCCGAGGGAT	ATGCAGACTG	240
GGAAGACGCC	GAAGACTATG	ACGACTATGAG	CGACTATGAG	GCCGCAGACC	AGGAGGCCGC	300
ACGGTGGCA	TCCTGGCAG	GGCGCTTGGC	GGTGCCTGTTA	CCAGACTGT	CCACGATTG	360
CATGGCGGCC	GCAGTCGTCA	TCATCTGCGG	CTTCACCGGG	CTCAGCGGAT	ACATTGTG	420
GCAACACCAT	GAGGCCACCG	AACGCCAGCA	GCGGCCGCGC	GCGTCGCCG	CCGGAGCCAA	480
GCAAGGTGTC	ATCAACATGA	CCTCGCTGGA	CTTCACAAAG	GCCAAAGAAG	ACGTCGGCGG	540
TGTGATCGC	AGCTCCACCG	CGCAATTCTAG	GGATGACTTC	CAGCAGCGGG	CAGCCGATTT	600
CACCAAGGTT	GTGCGAACAGT	CTAAAGTTGT	CACCGAAGGC	ACGGTGAACG	CGACAGCCGT	660
CGAATCCATG	AACGAGCAT	CCGCGTGGT	GCTCGTCGCG	GCGACTTCAC	GGGTCAACCAA	720
TTCCGCTGGG	GCGAAAGACG	AACCACGTG	GTGGCGGCTC	AAAGTGACCG	TGACCGAAGA	780
GGGGGGACAG	TACAAGATGT	CGAAAGTTGA	GTTCTGACCG	TGACCGATGA	CGTACGCGAC	840
GTCAACACCG	AAACCACTGA	GCCCCACCGA	GTCGCTGAGA	TCGACTCAGC	CGCAGGGGAA	900
GCCGGTGTATT	CGCGCACCGA	GGCATTGAC	ACCGACTCTG	CAACGGAATC	TACCGCGCAG	960
AAGGGTCAGC	GGCACCGTGA	CCTGTGGCGA	ATGCAGGTGA	CCTTGAAACC	CGTTCCGGTG	1020
ATTCTCATCC	TGCTCATGTT	GATCTCTGGG	GGCGCGACGG	GATGGCTATA	CCTTGAGCAA	1080
TACGACCCGA	TCAGCAGACG	GACTCCGGCG	CCGCCCCGTC	TGCCGTGCC	GGGGCGTCTG	1140
ACGGGACAAT	CGCGCTGTTG	TGTATTCA	CGACACGTCG	ACCAAGACTT	CGCTACCGCC	1200

AGGTCGCACC	TCGCCGGCGA	TTTCCGTGCC	TATACGACCA	GTTCACGCAG	CAGATCGTGG	1260
CTCCGGCGC	CAAACAGAAG	TCACTGAAAAA	CCACCGCCAA	GGTGGTCCGC	GC GGCCGTGT	1320
CGGAGCTACA	TCCGGATTCTG	GCCGTCGTT	TGGTTTTGT	CGACCAGAGC	ACTACCAGTA	1380
AGGACAGCCC	CAATCCGTCG	ATGGCGGCCA	GCAGCGTGT	GGTGACCCTA	GCCAAGGTCG	1440
ACGGCAATTG	GCTGATCACC	AAGTTCACCC	CGGTTTAGGT	TGCGCTAGGC	GGTCGCGAAG	1500
TCTGACGGGG	GCGCGGGTGG	CTGCTCGTGC	GAGATACCGG	CCGTTCTCG	GACAATCACG	1560
GCCCCACCTC	AAACAGATCT	CGGCCGCTGT	CTAATCGGCC	GGGTTATTAA	AGATTAGTTG	1620
CCACTGTATT	TACCTGTATG	TCAGATTGTT	CAGCTGGATT	TAGCTTCGCG	GCAGGGCGGC	1680
TGGTGCACCT	TGCATCTGGG	GTTGTGACTA	CTTGAGAGAA	TTTGACCTGT	TGCGGACGTT	1740
GTTTGCCTGC	CATCATTTGGT	GCTAGTTATG	GCCGAGCGGA	AGGATTATCG	AA GTGGTGGGA	1800
CTTCGGGGCG	TTACCAACCGG	AGATCAACTC	CGCGAGGATG	TACGCGGCC	CGGGTCTGGC	1860
CTCGCTGGTG	GCGCGCGCGA	AGATGTGGGA	CAGCGTGGCG	AGTGACCTGT	TTTCGGCCGC	1920
GTCGGCGTTT	CAGTCGGTGG	TCTGGGGTCT	GACGACGGGA	TCGTGGATAG	GTTCGTCGGC	1980
GGGTCTGATG	GTGGCGCGG	CCTCGCCGTA	TGTGGCGTGG	ATGAGCGTCA	CCGCGGGGCA	2040
GGCCGAGCTG	ACCGCCCGCC	AGGTCCGGGT	TGCTCGCGCG	GCCTACGAGA	CGGCGTATGG	2100
GCTGACCGTG	CCCCCGCGG	TGATCGCCGA	GAACCGTGT	GAACTGATGA	TTCTGATAGC	2160
GACCAACCTC	TTGGGGCAA	ACACCCCGC	GATCGCGGTC	AACGAGGCCG	AAATACGGGGA	2220
GATGTGGGCC	CAAGACCGCG	CCGCGATGTT	TGGCTACGCC	GCCACGGCGG	CGACGGCGAC	2280
CGAGGCCGTTG	CTGCCGTTCG	AGGACGCCCG	ACTGATCACC	AACCCCGCG	GGCTCTTGA	2340
GCAGGCCGTC	GC GGCGAGG	AGGCCATCGA	CACCGCCGCG	GCGAACCACT	TGATGAACAA	2400
TGTGCCCAA	GCGCTGCAAC	AACTGGCCA	GCCCACGAA	AGCATCTGGC	CGTTCGACCA	2460
ACTGAGTGAA	CTCTGGAAAG	CCATCTCGCC	GCATCTGTG	CCGCTCAGCA	ACATCGTGT	2520
GATGCTCAAC	AACCACGTGT	CGATGACCAA	CTCGGGTGTG	TCGATGGCCA	GCACCTTGC	2580
CTCAATGTTG	AAGGGCTTTG	CTCCGGCGGC	GGCTCAGGCC	GTGGAAACCG	CGGC GAAA	2640
CGGGTCCAG	GCGATGAGCT	CGCTGGCGAG	CCAGCTGGGT	TCGTGCGTGG	GTTCCTCGGG	2700
TCTGGGCCT	GGGGTGGCGG	CCAACTTGGG	TCGGGGCGCC	TCGGTCGGTT	CGTTGTGGT	2760
GCCGCAGGCC	TGGGCCGCGG	CCAAACCAGGC	GGTCACCCCG	GC GGCGCGGG	CGCTGCCGCT	2820

GACCAGCCTG ACCAGCGCCG CCCAAACCGC CCCCGGACAC ATGCTGGCG GGCTACCGCT	2880
GGGGCAACTG ACCAATAGCG GCGCGGGTT CGGGGGGTT AGCAATGGT TGCGGATGCC	2940
GCCGCGGGCG TACGTAATGC CCCGTGTGCC CGCCGCGGG TAACGCGAT CCGCACGCAA	3000
TGCGGGCCCT CTATGCGGGC AGCGATC	3027

## (2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 396 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Val Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met	
1 5 10 15	
Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Lys Met Trp	
20 25 30	
Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser	
35 40 45	
Val Val Trp Gly Leu Thr Thr Gly Ser Trp Ile Gly Ser Ser Ala Gly	
50 55 60	
Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr	
65 70 75 80	
Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala	
85 90 95	
Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala	
100 105 110	
Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly	
115 120 125	
Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met	
130 135 140	
Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Thr Ala Ala	
145 150 155 160	
Thr Ala Thr Glu Ala Leu Leu Pro Phe Glu Asp Ala Pro Leu Ile Thr	
165 170 175	
Asn Pro Gly Gly Leu Leu Glu Gln Ala Val Ala Val Glu Glu Ala Ile	
180 185 190	
Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu	

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195	200	205
Gln Gln Leu Ala Gln Pro Thr Lys Ser Ile Trp Pro Phe Asp Gln Leu		
210	215	220
Ser Glu Leu Trp Lys Ala Ile Ser Pro His Leu Ser Pro Leu Ser Asn		
225	230	235
Ile Val Ser Met Leu Asn Asn His Val Ser Met Thr Asn Ser Gly Val		
245	250	255
Ser Met Ala Ser Thr Leu His Ser Met Leu Lys Gly Phe Ala Pro Ala		
260	265	270
Ala Ala Gln Ala Val Glu Thr Ala Ala Gln Asn Gly Val Gln Ala Met		
275	280	285
Ser Ser Leu Gly Ser Gln Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu		
290	295	300
Gly Ala Gly Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser		
305	310	315
Leu Ser Val Pro Gln Ala Trp Ala Ala Asn Gln Ala Val Thr Pro		
325	330	335
Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Gln Thr		
340	345	350
Ala Pro Gly His Met Leu Gly Gly Leu Pro Leu Gly Gln Leu Thr Asn		
355	360	365
Ser Gly Gly Gly Phe Gly Gly Val Ser Asn Ala Leu Arg Met Pro Pro		
370	375	380
Arg Ala Tyr Val Met Pro Arg Val Pro Ala Ala Gly		
385	390	395

## (2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1616 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CATCGGAGGG AGTGATCAC C ATGCTGTGGC ACGCAATGCC ACCGGAGTAA ATACCGCAGC	60
GCTGATGGCC GGC GCGGGTC CGGCTCAA T GCTTGCGGGCG GCGCGGGAT GGCAGACGCT	120
TTCCGGGGCT CTGGACGCTC AGGCCGTGCA GTTGACCGCG CGCCTGAACT CTCTGGGAGA	180
AGCCTGGACT GGAGGTGGCA GCGACAAGGC GCTTGCGGGCT GCAACGCCGA TGGTGGTCTG	240

GCTACAAACC GCGTCAACAC AGGCCAAGAC CCGTGCATG CAGGCGACGG CGCAAGCCGC 300  
 GGCATACACC CAGGCCATGG CCACGACGCC GTCGCTGCCG GAGATGCCG CCAACCACAT 360  
 CACCCAGGCC GTCCTTACGG CCACCAACTT CTTCGGTATC AACACGATC CGATCGCGTT 420  
 GACCGAGATG GATTATTCA TCCGTATGTG GAACCAGGCA GCCCTGGCAA TGGAGGTCTA 480  
 CCAGGCCAG ACCGCCGTTA ACACGCTTT CGAGAACGTC GAGGCCATGG CGTCGATCCT 540  
 TGATCCCGC GCGAGCCAGA GCACGACGAA CCCGATCTTC GGAATGCCCT CCCCTGGAG 600  
 CTCAACACCG GTTGGCCAGT TGCCGCCGGC GGCTACCCAG ACCCTCGGCC AACTGGGTGA 660  
 GATGAGGGC CCGATGCAAG AGCTGACCCA GCGCTGCAG CAGGTGACGT CGTTGTTCAAG 720  
 CCAGGTGGC GGCACCGGCC GCGGCAACCC AGCCGACGAG GAAGCCGCAG AGATGGGCCT 780  
 GCTCGGCACC AGTCCGCTGT CGAACCATCC GCTGGCTGT GGATCAGGCC CCAGCGCGG 840  
 CGCGGGCTG CTGCGCCCG AGTCGCTACC TGGCGCAGGT GGGTCGTTGA CCCGCACGCC 900  
 GCTGATGTCT CAGCTGATCG AAAAGCCGGT TGCCCCCTCG GTGATGCCGG CGGCTGCTGC 960  
 CGGATCGCTG GCGACGGGTG GCGCCGCTCC GGTGGGTGCG GGAGCGATGG GCCAGGGTGC 1020  
 GCAATCCGCC GGCTCCACCA GGCGGGTCT GGTCGCGCCG GCACCGCTCG CGCAGGAGCG 1080  
 TGAAGAACAC GACGAGGACG ACTGGGACGA AGAGGACGAC TGGTGAGCTC CCGTAATGAC 1140  
 AACAGACTTC CGGCCACCC GGCGCGGAAG ACTTGCCAAC ATTTTGGCGA GGAAGGTTAA 1200  
 GAGAGAAAGT AGTCGACAT GGCAGAGATG AAGACCGATG CGCCTACCC CGCGCAGGAG 1260  
 GCAGGTAATT TCGAGCGGAT CTCCGGCGAC CTGAAAACCC AGATCGACCA GGTGGAGTCG 1320  
 ACGGCAGGT CGTTGCAAGG CCAGTGGCGC GCGCGCGCGG GGACGCCGC CGAGGCCGCG 1380  
 GTGGTGCCTG TCCAAGAACG AGCCAATAAG CAGAAGCAGG AAATCGACGA GATCTCGACG 1440  
 AATATTCGTC AGGCCGGCGT CCAATACTCG AGGGCCGACG AGGAGCAGCA GCAGGGCTG 1500  
 TCCTCGCAA TGGCTTCTG ACCCGCTAAT ACGAAAAGAA ACGGAGCAAA AACATGACAG 1560  
 AGCAGCAGTG GAATTCGCG GGTATCGAGG CGCGGGCAAG CGCAATCCAG GGAAAT 1616

## (2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CTAGTGGATG GGACCATGGC CATTTCCTGC AGTCTCACTG CCTTCTGTGT TGACATTTG	60
GCACGCCGGC GGAAACGAAG CACTGGGTC GAAGAACGGC TCGCGCTGCCA TATCGTCCGG	120
AGCTTCCATA CCTTCGTGCG GCCGGAAGAG CTTGTCGTAG TCGGCGGCCA TGACAACTC	180
TCAGAGTGGC CTCAAACGTA TAAACACGAG AAAGGGCGAG ACCGACGGA GGTCGAACTC	240
GCCCCATCCC GTGTTCGCT ATTCTACGCG AACTCGGCGT TGCCCTATGC GAACATCCCA	300
GTGACGTTGC CCTCGGTGCA AGCCATTGCC TGACCGGCTT CGCTGATCGT CGCGGCCAGG	360
TTCTGCAAGCG CGTGTTCAG CTCGGTAGCC GTGGCGTCCC ATTTTGCTG GACACCCCTGG	420
TACGCCCTCG AA	432

## (2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Leu Trp His Ala Met Pro Pro Glu Xaa Asn Thr Ala Arg Leu Met			
1	5	10	15
Ala Gly Ala Gly Pro Ala Pro Met Leu Ala Ala Ala Ala Gly Trp Gln			
20	25	30	
Thr Leu Ser Ala Ala Leu Asp Ala Gln Ala Val Glu Leu Thr Ala Arg			
35	40	45	
Leu Asn Ser Leu Gly Glu Ala Trp Thr Gly Gly Ser Asp Lys Ala			
50	55	60	
Leu Ala Ala Ala Thr Pro Met Val Val Trp Leu Gln Thr Ala Ser Thr			
65	70	75	80
Gln Ala Lys Thr Arg Ala Met Gln Ala Thr Ala Gln Ala Ala Tyr			
85	90	95	
Thr Gln Ala Met Ala Thr Thr Pro Ser Leu Pro Glu Ile Ala Ala Asn			
100	105	110	
His Ile Thr Gln Ala Val Leu Thr Ala Thr Asn Phe Phe Gly Ile Asn			
115	120	125	
Thr Ile Pro Ile Ala Leu Thr Glu Met Asp Tyr Phe Ile Arg Met Trp			
130	135	140	

Asn Gln Ala Ala Leu Ala Met Glu Val Tyr Gln Ala Glu Thr Ala Val  
 145 150 155 160  
 Asn Thr Leu Phe Glu Lys Leu Glu Pro Met Ala Ser Ile Leu Asp Pro  
 165 170 175  
 Gly Ala Ser Gln Ser Thr Thr Asn Pro Ile Phe Gly Met Pro Ser Pro  
 180 185 190  
 Gly Ser Ser Thr Pro Val Gly Gln Leu Pro Pro Ala Ala Thr Gln Thr  
 195 200 205  
 Leu Gly Gln Leu Gly Glu Met Ser Gly Pro Met Gln Gln Leu Thr Gln  
 210 215 220  
 Pro Leu Gln Gln Val Thr Ser Leu Phe Ser Gln Val Gly Gly Thr Gly  
 225 230 235 240  
 Gly Gly Asn Pro Ala Asp Glu Glu Ala Ala Gln Met Gly Leu Leu Gly  
 245 250 255  
 Thr Ser Pro Leu Ser Asn His Pro Leu Ala Gly Gly Ser Gly Pro Ser  
 260 265 270  
 Ala Gly Ala Gly Leu Leu Arg Ala Glu Ser Leu Pro Gly Ala Gly Gly  
 275 280 285  
 Ser Leu Thr Arg Thr Pro Leu Met Ser Gln Leu Ile Glu Lys Pro Val  
 290 295 300  
 Ala Pro Ser Val Met Pro Ala Ala Ala Gly Ser Ser Ala Thr Gly  
 305 310 315 320  
 Gly Ala Ala Pro Val Gly Ala Gly Ala Met Gly Gln Gly Ala Gln Ser  
 325 330 335  
 Gly Gly Ser Thr Arg Pro Gly Leu Val Ala Pro Ala Pro Leu Ala Gln  
 340 345 350  
 Glu Arg Glu Glu Asp Asp Glu Asp Asp Trp Asp Glu Glu Asp Asp Trp  
 355 360 365

## (2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Met Ala Glu Met Lys Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly  
 1 5 10 15

Asn Phe Glu Arg Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val  
 20 25 30

Glu Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly  
 35 40 45

Thr Ala Ala Gln Ala Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys  
 50 55 60

Gln Lys Gln Glu Leu Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly  
 65 70 75 80

Val Gln Tyr Ser Arg Ala Asp Glu Glu Gln Gln Ala Leu Ser Ser  
 85 90 95

Gln Met Gly Phe  
 100

## (2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GATCTCCGGC GACCTGAAAA CCCAGATCGA CCAGGTGGAG TCGACGGCAG GTTCGTTGCA	60
GGGCCAGTGG CGCGGCCGG CGGGGACGGC CGCCCAGGCC GCGGTGGTGC GCTTCCAAGA	120
AGCAGCCAAT AACGAGAACG AGGAACCTCGA CGAGATCTCG ACGAATATTC GTCAGGCCGG	180
CGTCCAATAC TCGAGGGCCG ACGAGGAGCA GCAGCAGGCC CTGTCCTCGC AAATGGGTT	240
CTGACCCGCT AATACGAAAA GAAACGGAGC AAAACATGA CAGAGCAGCA GTGGAATTTC	300
GGGGGTATCG AGGCCGCCGG AAGCGCAATC CAGGGAAATG TCACGTCCAT TCATTCCCTC	360
CTTGACGAGG GGAAGCAGTC CCTGACCAAG CTCGCA	396

## (2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala	
1 5 10 15	

Gly Ser Leu Gln Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln  
 20 25 30

Ala Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu  
 35 40 45

Leu Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser  
 50 55 60

Arg Ala Asp Glu Glu Gln Gln Ala Leu Ser Ser Gln Met Gly Phe  
 65 70 75 80

## (2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GTGGATCCCG ATCCCGTGT TCGCTATTCT ACGCGAACCTC GGCCTTGCCC TATGCGAACAA 60  
 TCCCAGTGAC GTTGCTTCG GTCGAAGCCA TTGCTGACCC GGCTTCGCTG ATCGTCGCG 120  
 CCAGGTTCTG CAGCGCGTTG TTCAGCTCG TAGCCGTGTC GTCCCATTTC TGCTGGACAC 180  
 CCTGGTACGC CTCCGAACCG CTACCGCCCC AGGCCGCTGC GAGCTTGGTC AGGGACTGCT 240  
 TCCCCTCGTC AAGGAGGGAA TGAATGGACG TGACATTTCC CTGGATTGCG CTTGCCGCGG 300  
 CCTCGATACC CGCGAAATTC CACTGCTGCT CTGTCATGTT TTTGCTCCGT TTCTTTTCGT 360  
 ATTAGCGGGT CAGAAGCCCCA TTTGCGA 387

## (2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CGGCACGAGG ATCTCGGGTG GCCCAACCGC GCTGGCGAGG GCTCCGTTCC GGGGGCGAGC 60  
 TGGCGCCCGG ATGCTTCCTC TGCCCGCAGC CGCCGCTGGA TGGATGGACC AGTTGCTACC 120  
 TTCCCGACGT TTGCTGCGGT GTCTGTGCGA TAGCGGGTAC CCCGGCGCGC ACGTCGGGAG 180  
 TGTGGGGGG CAGGCCGGGT CGGTGGTTCG GCCGGGGACG CAGACGGTCT GGACCGAACG 240

GGCGGGGGTT CGCCGATTGG CATCTTGCC CA

272

## (2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Asp	Pro	Val	Asp	Ala	Val	Ile	Asn	Thr	Thr	Cys	Asn	Tyr	Gly	Gln	Val
1															15
Val Ala Ala Leu															
				20											

## (2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Ala	Val	Glu	Ser	Gly	Met	Leu	Ala	Leu	Gly	Thr	Pro	Ala	Pro	Ser
1														15
5														

## (2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Ala	Ala	Met	Lys	Pro	Arg	Thr	Gly	Asp	Gly	Pro	Leu	Glu	Ala	Ala	Lys
1															15
5															
Glu Gly Arg															

## (2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp Pro Ala Trp Gly Pro  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Asp Ile Gly Ser Glu Ser Thr Glu Asp Gln Gln Xaa Ala Val  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Ala Glu Glu Ser Ile Ser Thr Xaa Glu Xaa Ile Val Pro  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Asp Pro Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro  
 1 5 10 15

Ser

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Ala	Pro	Lys	Thr	Tyr	Xaa	Glu	Glu	Leu	Lys	Gly	Thr	Asp	Thr	Gly
1					5				10				15	

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Asp	Pro	Ala	Ser	Ala	Pro	Asp	Val	Pro	Thr	Ala	Ala	Gln	Leu	Thr	Ser
1						5				10				15	
Leu	Leu	Asn	Ser	Leu	Ala	Asp	Pro	Asn	Val	Ser	Phe	Ala	Asn		
				20				25					30		

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Asp	Pro	Pro	Asp	Pro	His	Gln	Xaa	Asp	Met	Thr	Lys	Gly	Tyr	Tyr	Pro
1						5			10				15		
Gly	Gly	Arg	Arg	Xaa	Phe										
				20											

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Asp	Pro	Gly	Tyr	Thr	Pro	Gly
1					5	

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:  
(D) OTHER INFORMATION: /note= "The Second Residue Can Be Either a Pro or Thr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Xaa Xaa Gly Phe Thr Gly Pro Gln Phe Tyr  
1 5 10

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ix) FEATURE:  
(D) OTHER INFORMATION: /note= "The Third Residue Can Be Either a Gln or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Xaa Pro Xaa Val Thr Ala Tyr Ala Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Xaa Xaa Xaa Glu Lys Pro Phe Leu Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Xaa Asp Ser Glu Lys Ser Ala Thr Ile Lys Val Thr Asp Ala Ser  
1 5 10 15

(2) INFORMATION FOR SEO ID NO:135:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Ala Gly Asp Thr Xaa Ile Tyr Ile Val Gly Asn Leu Thr Ala Asp  
1 5 10 15

(2) INFORMATION FOR SEO ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Xaa Tyr Ile Ala Tyr Xaa Thr Thr Ala Gly Ile Val Pro Gly Lys Ile  
1 5 10 15

Asn Val His Leu Val  
20

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 882 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GCAACGCTGT	CGTGGCTTT	GCGGTGATCG	GTTTCGCCTC	GCTGGCGGTG	GCGGTGGCGG	60
TCACCATCCG	ACCGACCGCG	GCCTCAAAAC	CGCTAGAGGG	ACACCAAAAC	GCCCAGCCAG	120
GGAAGTTCAT	GCCGTTGTTG	CGGACGCAAC	AGCAGGCGCC	GGTCCCCTCG	CCTCCGCCG	180
ATGATCCAC	CGCTGGATTG	CAGGGCGGCA	CCATTCCCGG	TGTACAGAAC	GTGGTGCCTG	240
GCCCCGGTAC	CTCACCCGGG	GTGGGTTGGA	CGCCGGCTTC	GCCTGGCGCG	GAAGCGCCGG	300
CCGTGCCCGG	TGTTGTGCCT	CCCCGGTGC	CAATCCCGT	CCCGATCATC	ATTCCCCGT	360
TCCCCGGTTG	CGACGCTGGA	ATGCGGACCA	TCCCCACCGC	ACCGCCGACG	ACGCCGGTGA	420
CCACGTCGGC	GACGACGGCG	CGGACCAACG	CGCCGACCCAC	GCGGTGACCC	ACGCCGCCAA	480
CGACGCCGCC	GACCACGCCG	GTGACCAACG	CGCCAAACGAC	GCCGCGGACC	ACGCCGGTGA	540
CCACGCCACC	AACGACCGTC	CCCCGACGA	CCGTCGCCCC	GACGACGGTC	GCTCCGACCA	600
CCGTGCCCGG	GACCACGGTC	GTCAGGCCA	CCGCCACGCC	GACGACGGTC	GCTCCGACGC	660
CGACCGAGCA	CCCCACGCA	CAACCAACCC	AACAGATGCC	AACCCAGCAG	CAGACCGTGG	720
CCCCGAGAC	GGTGGCGCCG	GTCAGGCCG	CGCCGTCGCG	TGGCCGACCA	GGCAGCGGCG	780
GGGGCGACTT	ATTGCGCGG	TTCTGATCAC	GGTGGCGGCT	TCACTACGGT	CGGAGGACAT	840
GGCCGGTGT	GCGGTGACGG	TGGTGCCTGC	CTGTCTAAC	GA		882

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

CCATCAACCA	ACCGCTCGCG	CGCCCGCGC	CGCCGGATCC	GCGTCGCGG	CCACGCCCGC	60
CGGTGCCCTC	GGTGGCCCGG	TTGCGCCGCT	CGCCGCCGTC	GCCGCCGACC	GGCTGGGTGC	120
CTAGGGCGCT	GTTACCGCCC	TGGTTGGCGG	GGACGCCGCC	GGCACCAACG	GTACCGCCGA	180
TGGCGCCGTT	GGCGCCGGCG	GCACCGTTGC	CACCGTTGCC	ACCGTTGCCA	CGCTTGCCGA	240
CCAGGCCACCC	CCCGCGACCA	CCGGCACCGC	CGCCGCCGCC	CGCACCGCCG	GGGTGCCCGT	300
TCGTGCCCGT	ACCGCCGGCA	CCGCGCTTGC	CGCGGTCA	GCCGACGGAA	CTACCGGGCG	360
ACGCGGGCTG	CCCGCCGGCG	CGCCGCCAC	CGCCATTGGC	ACCGCCGTCA	CGCCGGCTG	420

GGAGTGCAGC GATTAGGGCA CTGACCGGGCG CAACCAGCGC AAGTACTCTC GGTCACCGAG	480
CACTTCCAGA CGACACCACA GCACGGGGTT GTCGGCGGAC TGGGTGAAAT GGCAGCCGAT	540
AGCGGCTAGC TGTCGGCTGC GGTCAACCTC GATCATGATG TCGAGGTGAC CGTGACCGCG	600
CCCCCGGAAG GAGGCCTGAG ACTCGGGCTT GAGCCGATCG GCGATCGGTT GGGGCAGTGC	660
CCAGGGCAAT ACGGGGATAC CGGGTGTCTNA AGCCGCCGCG AGCGCAGCTT CGGTTGCCGCG	720
ACNGTGTCTG GGGTGGCTG TTACGCCGTT GTCNTCGAAC ACGAGTAGCA GGTCTGCTCC	780
GGCGAGGGCA TCCACCAACGC GTTGCCTGAG CTCGTT	840

## (2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1152 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

ACCAGCCGCC GGCTGAGGTC TCAGATCAGA GAGTCTCCGG ACTCACCAGG GCGGGTTCAGC	60
CTTCTCCAG AACAACTGCT GAAGATCCTC GCCCGCGAAA CAGGCCTGTA TTTGACGCTC	120
TATGACCGGT TGAACGACGA GATCATCCGG CAGATTGATA TGGCACCGCT GGGCTAACAG	180
GTGCGCAAGA TGGTGCAGCT GTATGCTCTG GACTCCGTGT CGCGGATCAG CTTTGGCAGC	240
GGCCGGGTGA TCGTGTGGAG CGAGGAGCTC GGCAGAGGCC AGTATCCGAT CGAGACGCTG	300
GACGGCATCA CGCTGTTGG GCGGCCGACG ATGACAAACGC CCTTCATCGT TGAGATGCTC	360
AAGCGTGTGAGC GCGACATCCA GCTCTTCACG ACCGACGCC ACTACCAGGG CGGGATCTCA	420
ACACCCGACG TGTCTACGC GCGCGGCTC CGTCAGCAAG TTCAACCGAC CGACGATCCT	480
GCGTTCTGCC TGTCTGTTAAAG CAAGCGGATC GTGTCGAGGA AGATCCTGAA TCAGCAGGCC	540
TTGATTCCGG CACACACGTC GGGGCAAGAC GTTGCTGAGA GCATCCGCAC GATGAAGCAC	600
TCGCTGGCCT GGGTCGATCG ATCGGGCTCC CTGGCGGAGT TGAACGGGTT CGAGGGAAAT	660
GCCGAAAGG CATACTTCAC CGCGCTGGGG CATCTCGTC CGCAGGAGTT CGCATTCCAG	720
GGCCGCTCGA CTCGGCCGCC GTTGGACGCC TTCAACTCGA TGGTCAGGCC CGGCTATTCTG	780
CTGCTGTACA AGAACATCAT AGGGCGATC GAGCGTCACA GCCTGAACGC GTATATCGGT	840

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TTCCTACACC AGGATTACAG AGGGCACGCA ACGTCTCGTG CGGAATTCCG CACGAGCTCC	900
GCTGAAACCG CTGGCCGGCT GCTCAGTGC CGTACGTAAT CGCCTGCGCC CAGGCCGGCC	960
CGCCGGCCGA ATACCAGCAG ATCGGACAGC GAATTGCCGC CCAGCCGGTT GGAGCCGTGC	1020
ATACCGCCGG CACACTCACC GGCGACGAAC AGGCCTGGCA CGTGGCGGC GCCGGTGTCC	1080
GCGTCTACTT CGACACCGCC CATCACCTAG TGACACGTCG GCCCCACTTC CATTGCGTGC	1140
GTTCGGCACG AG	1152

## (2) INFORMATION FOR SEQ ID NO:141:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 655 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

CTCGTGCAGA TTGGCAGGG TGTACTTGCC GGTGGGTGAT GCGCATGAG TGCCGACGAC	60
CAGCAATGCG GCAACAGCAG GGATCCCGGT CAACGACGCC ACCGGTCCA CGTGGGGAT	120
CCGCTCGAGT CCGCCCTGGG CGGCTCTTTC CTTGGCAGG GTCATCCGAC GTGTTTCCGC	180
CGTGGTTTGC CGCCATTATG CGGGCGCGC GCGTCGGCGC GCGGTATGG CGGAANGTCG	240
ATCAGCACAC CGAGATAAG GGTCTGTGCA AGCTTTTGA GCGTCGGCG GGGCAGCTTC	300
GCCGGCAATT CTACTAGCGA GAAAGTCTGGC CCGATACGGA TCTGACCGAA GTCGCTGCGG	360
TGCAGCCCAC CCTCATGGC GATGGCGCG ACGATGGCGC CTGGACCGAT CTTGTGCGC	420
TTGCCGACGG CGACGGGTA GGTGGTCAAG TCCGGTCTAC GCTTGGGCCT TTGCGGACGG	480
TCCCGACGCT GGTGCGGGTT GCGCCGGAA AGCGGGGGGT CGGGTCCAT CAGGAATGCC	540
TCACCGCCGC GGCACGTGAC GGCGAGTGC GCGGCGATGT CAGCCATCGG GACATCATGC	600
TCGGGTTCAT ACTCCTCGAC CAGTCGGCGG AACAGCTCGA TTCCCGGACC GCCCA	655

## (2) INFORMATION FOR SEQ ID NO:142:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Asn Ala Val Val Ala Phe Ala Val Ile Gly Phe Ala Ser Leu Ala Val			
1	5	10	15
Ala Val Ala Val Thr Ile Arg Pro Thr Ala Ala Ser Lys Pro Val Glu			
20	25	30	
Gly His Gln Asn Ala Gln Pro Gly Lys Phe Met Pro Leu Leu Pro Thr			
35	40	45	
Gln Gln Gln Ala Pro Val Pro Pro Pro Pro Asp Asp Pro Thr Ala			
50	55	60	
Gly Phe Gln Gly Gly Thr Ile Pro Ala Val Gln Asn Val Val Pro Arg			
65	70	75	80
Pro Gly Thr Ser Pro Gly Val Gly Gly Thr Pro Ala Ser Pro Ala Pro			
85	90	95	
Glu Ala Pro Ala Val Pro Gly Val Val Pro Ala Pro Val Pro Ile Pro			
100	105	110	
Val Pro Ile Ile Ile Pro Pro Phe Pro Gly Trp Gln Pro Gly Met Pro			
115	120	125	
Thr Ile Pro Thr Ala Pro Pro Thr Thr Pro Val Thr Thr Ser Ala Thr			
130	135	140	
Thr Pro Pro Thr Thr Pro Pro Thr Thr Pro Val Thr Thr Pro Pro Thr			
145	150	155	160
Thr Pro Pro Thr Thr Pro Val Thr Thr Pro Pro Thr Thr Pro Pro Thr			
165	170	175	
Thr Pro Val Thr Thr Pro Pro Thr Thr Val Ala Pro Thr Thr Val Ala			
180	185	190	
Pro Thr Thr Val Ala Pro Thr Thr Val Ala Pro Thr Thr Val Ala Pro			
195	200	205	
Ala Thr Ala Thr Pro Thr Thr Val Ala Pro Gln Pro Thr Gln Gln Pro			
210	215	220	
Thr Gln Gln Pro Thr Gln Gln Met Pro Thr Gln Gln Gln Thr Val Ala			
225	230	235	240
Pro Gln Thr Val Ala Pro Ala Pro Gln Pro Pro Ser Gly Gly Arg Asn			
245	250	255	
Gly Ser Gly Gly Gly Asp Leu Phe Gly Gly Phe			
260	265		

(2) INFORMATION FOR SEQ ID NO:143:

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Ile	Asn	Gln	Pro	Leu	Ala	Pro	Pro	Ala	Pro	Pro	Asp	Pro	Pro	Ser	Pro
1				5					10					15	
Pro	Arg	Pro	Pro	Val	Pro	Pro	Val	Pro	Pro	Leu	Pro	Pro	Ser	Pro	Pro
	20						25						30		
Ser	Pro	Pro	Thr	Gly	Trp	Val	Pro	Arg	Ala	Leu	Leu	Pro	Pro	Trp	Leu
	35					40						45			
Ala	Gly	Thr	Pro	Pro	Ala	Pro	Pro	Val	Pro	Pro	Met	Ala	Pro	Leu	Pro
	50					55					60				
Pro	Ala	Ala	Pro	Leu	Pro	Thr									
	65				70				75				80		
Ser	His	Pro	Pro	Arg	Pro	Pro	Ala	Pro	Pro	Ala	Pro	Pro	Ala	Pro	Pro
	85						90					95			
Ala	Cys	Pro	Phe	Val	Pro	Pro	Ala	Pro	Pro	Leu	Pro	Pro	Ser		
	100					105					110				
Pro	Pro	Thr	Glu	Leu	Pro	Ala	Asp	Ala	Ala	Cys	Pro	Pro	Ala	Pro	Pro
	115						120					125			
Ala	Pro	Pro	Leu	Ala	Pro	Pro	Ser	Pro	Pro	Ala	Gly	Ser	Ala	Ala	Ile
	130					135					140				
Arg	Ala	Leu	Thr	Gly	Ala	Thr	Ser	Ala	Ser	Thr	Leu	Gly	His	Arg	Ala
	145						150				155			160	
Leu	Pro	Asp	Asp	Thr	Thr	Ala	Arg	Gly	Cys	Arg	Arg	Thr	Gly		
						165			170						

## (2) INFORMATION FOR SEQ ID NO:144:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Gln Pro Pro Ala Glu Val Ser Asp Gln Arg Val Ser Gly Leu Thr Gly  
 1 5 10 15

Ala Val Gln Pro Ser Pro Arg Thr Thr Ala Glu Asp Pro Arg Pro Arg  
 20 25 30

Asn Arg Arg  
 35

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Arg Ala Asp Ser Ala Gly Cys Thr Cys Arg Trp Cys Xaa Pro His Glu  
 1 5 10 15

Cys Arg Arg Pro Ala Met Arg Gln Gln His Gly Ser Arg Ser Thr Thr  
 20 25 30

Pro Pro Gly Pro Arg Gly Arg Ser Ala Arg Val Arg Pro Gly Arg Leu  
 35 40 45

Phe Pro Trp Ala Gly Ser Ser Asp Val Phe Pro Pro Trp Phe Ala Ala  
 50 55 60

Ile Met Pro Ala Arg Arg Val Gly Arg Pro Val Trp Pro Xaa Val Asp  
 65 70 75 80

Gln His Thr Arg Asp Thr Gly Leu Cys Lys Leu Phe Glu Arg Arg Ala  
 85 90 95

Gly Gln Leu Arg Arg Gln Phe Tyr  
 100

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

205220-348480001

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GGATCCATAT GGGCCATCAT CATCATCATC ACGTGATCGA CATCATCGGG ACC

53

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR Primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CCTGAATTCA GGCTCGGTT GCGCCGGCCT CATCTTGAAC GA

42

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR Primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GGATCTGCA GGCTCGAAC CACCGAGCGG T

31

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

100084813 - 0222502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

CTCTGAATTC AGCGCTGGAA ATCGTCGCGA T 31

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GGATCCAGCG CTGAGATGAA GACCGATGCC GCT 33

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GAGAGAATTC TCAGAAGCCC ATTTGCGAGG ACA 33

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(ix) FEATURE:

202520 - 202520 - 202520 - 202520 - 202520

(A) NAME/KEY: CDS  
 (B) LOCATION: 152..1273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

TGTTCTTCGA CGGCAGGCTG GTGGAGGAAG GGCCCACCGA ACAGCTGTTG TCCTCGCCGA	60
AGCATGCGGA AACCGCCCGA TACGTCGCCG GACTGTCGGG GGACGTCAG GACGCCAACG	120
GCAGAAATTG AAGAGCACAG AAAGGTATGG C GTG AAA ATT CGT TTG CAT ACG	172
Val Lys Ile Arg Leu His Thr	
1 5	
CTG TTG GCC GTG TTG ACC GCT GCG CCG CTG CTG CTA GCA GCG GCG GGC	220
Leu Leu Ala Val Leu Thr Ala Ala Pro Leu Leu Leu Ala Ala Ala Gly	
10 15 20	
TGT GGC TCG AAA CCA CCG AGC GGT TCG CCT GAA ACG GGC GCC GGC GGC	268
Cys Gly Ser Lys Pro Pro Ser Gly Ser Pro Glu Thr Gly Ala Gly Ala	
25 30 35	
GGT ACT GTC GCG ACT ACC CCC GCG TCG TCG CCG GTG ACG TTG GCG GAG	316
Gly Thr Val Ala Thr Thr Pro Ala Ser Ser Pro Val Thr Leu Ala Glu	
40 45 50 55	
ACC GGT AGC ACG CTG CTC TAC CCG CTG TTC AAC CTG TGG GGT CCG GCC	364
Thr Gly Ser Thr Leu Leu Tyr Pro Leu Phe Asn Leu Trp Gly Pro Ala	
60 65 70	
TTT CAC GAG AGG TAT CCG AAC GTC ACG ATC ACC GCT CAG GGC ACC GGT	412
Phe His Glu Arg Tyr Pro Asn Val Thr Ile Thr Ala Gln Gly Thr Gly	
75 80 85	
TCT GGT GCC GGG ATC GCG CAG GCC GCC GGG ACG GTC AAC ATT GGG	460
Ser Gly Ala Gly Ile Ala Gln Ala Ala Gly Thr Val Asn Ile Gly	
90 95 100	
GCC TCC GAC GCC TAT CTG TCG GAA GGT GAT ATG GCC GCG CAC AAG GGG	508
Ala Ser Asp Ala Tyr Leu Ser Glu Gly Asp Met Ala Ala His Lys Gly	
105 110 115	
CTG ATG AAC ATC GCG CTA GCC ATC TCC GCT CAG CAG GTC AAC TAC AAC	556
Leu Met Asn Ile Ala Leu Ala Ile Ser Ala Gln Gln Val Asn Tyr Asn	
120 125 130 135	
CTG CCC GGA GTG AGC GAG CAC CTC AAG CTG AAC GGA AAA GTC CTG GCG	604
Leu Pro Gly Val Ser Glu His Leu Lys Leu Asn Gly Lys Val Leu Ala	
140 145 150	
GCC ATG TAC CAG GGC ACC ATC AAA ACC TGG GAC GAC CCG CAG ATC GCT	652
Ala Met Tyr Gln Gly Thr Ile Lys Thr Trp Asp Asp Pro Gln Ile Ala	
155 160 165	
GCG CTC AAC CCC GGC GTG AAC CTG CCC GGC ACC GCG GTA GTT CCG CTG	700
Ala Leu Asn Pro Gly Val Asn Leu Pro Gly Thr Ala Val Val Pro Leu	

40081813 022502

170	175	180	
CAC CGC TCC GAC GGG TCC GGT GAC ACC TTC TTG TTC ACC CAG TAC CTG His Arg Ser Asp Gly Ser Gly Asp Thr Phe Leu Phe Thr Gln Tyr Leu 185	190	195	748
TCC AAG CAA GAT CCC GAG GGC TGG GGC AAG TCG CCC GGC TTC GGC ACC Ser Lys Gln Asp Pro Glu Gly Trp Gly Lys Ser Pro Gly Phe Gly Thr 200	205	210	215
ACC GTC GAC TTC CCG GCG GTG CCG GGT GCG CTG GGT GAG AAC GGC AAC Thr Val Asp Phe Pro Ala Val Pro Gly Ala Leu Gly Glu Asn Gly Asn 220	225	230	844
GCG GGC ATG GTG ACC GGT TGC GCC GAG ACA CCG GGC TGC GTG GCC TAT Gly Gly Met Val Thr Gly Cys Ala Glu Thr Pro Gly Cys Val Ala Tyr 235	240	245	892
ATC GGC ATC AGC TTC CTC GAC CAG GCC AGT CAA CGG GGA CTC GGC GAG Ile Gly Ile Ser Phe Leu Asp Gln Ala Ser Gln Arg Gly Leu Gly Glu 250	255	260	940
GCC CAA CTA GGC AAT AGC TCT GGC AAT TTC TTG TTG CCC GAC GCG CAA Ala Gln Leu Gly Asn Ser Ser Gly Asn Phe Leu Leu Pro Asp Ala Gln 265	270	275	988
AGC ATT CAG GCC GCG GCG GCT GGC TTC GCA TCG AAA ACC CCG GCG AAC Ser Ile Gln Ala Ala Ala Gly Phe Ala Ser Lys Thr Pro Ala Asn 280	285	290	295
CAG GCG ATT TCG ATG ATC GAC GGG CCC GCC CCG GAC GGC TAC CCG ATC Gln Ala Ile Ser Met Ile Asp Gly Pro Ala Pro Asp Gly Tyr Pro Ile 300	305	310	1084
ATC AAC TAC GAG TAC GCC ATC GTC AAC AAC CGG CAA AAG GAC GGC GCC Ile Asn Tyr Glu Tyr Ala Ile Val Asn Asn Arg Gln Lys Asp Ala Ala 315	320	325	1132
ACC GCG CAG ACC TTG CAG GCA TTT CTG CAC TGG GCG ATC ACC GAC GGC Thr Ala Gln Thr Leu Gln Ala Phe Leu His Trp Ala Ile Thr Asp Gly 330	335	340	1180
AAC AAG GCC TCG TTC CTC GAC CAG GTT CAT TTC CAG CCG CTG CCG CCC Asn Lys Ala Ser Phe Leu Asp Gln Val His Phe Gln Pro Leu Pro Pro 345	350	355	1228
GCG GTG GTG AAG TTG TCT GAC GCG TTG ATC GCG ACG ATT TCC AGC Ala Val Val Lys Leu Ser Asp Ala Leu Ile Ala Thr Ile Ser Ser 360	365	370	1273
TAGCCTCGTT GACCACCAAG CGACAGCAAC CTCCGTCGGG CCATCGGGCT GCTTTGCGGA GCATGCTGGC CCGTGCCGGT GAAAGTCGGCC GCGCTGGCC GGCCATCCGG TGGTTGGGTG GGATAGGTGCGT GGTGATCCCC CTGCTTGCAG TGGTCTTGGT GCTGGTGGTG CTGGTCATCG 1453			1333

AGGCAGATGGG	TGCGATCAGG	CTCAACGGGT	TGCATTTCTT	CACCGCCACC	GAATGGAATC	1513
CAGGCAACAC	CTACGGCGAA	ACCGTTGCTA	CCGACGCGTC	GCCCATCCGG	TCGGCGCTTA	1573
CTACGGGGCG	TTGCGCGTGA	TCGTCGGGAC	GCTGGCGACC	TCGGCAATCG	CCCTGATCAT	1633
CGCGGTGCGG	GTCTCTGTAG	GAGCGGCCTG	GGTGATCGTG	GAACGGCTGC	CGAAACGGTT	1693
GGCCGAGGCT	GTGGGAATAG	TCCTGGAATT	GCTCGCCGGA	ATCCCCAGCG	TGGTOGTCGG	1753
TTTGTGGGGG	GCAATGACGT	TCGGGCCGTT	CATCGCTCAT	CACATCGCTC	CGGTGATCGC	1813
TCACAACGCT	CCCGATGTC	CGGTGCTGAA	CTACTTGCGC	GGCGAACCCGG	GCAACGGGGA	1873
GGGCATGTTG	GTGTCCGGTC	TGGTGTGGC	GGTGATGGTC	GTTCCCATTA	TCGCCACCAC	1933
CACTCATGAC	CTGTTCCGGC	AGGTGCCGGT	GTTGCCCGG	GAGGGCGCGA	TCGGGAATTC	1993

## (2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 374 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Val	Lys	Ile	Arg	Leu	His	Thr	Leu	Leu	Ala	Val	Leu	Thr	Ala	Ala	Pro
1															15

Leu	Leu	Leu	Ala	Ala	Ala	Gly	Cys	Gly	Ser	Lys	Pro	Pro	Ser	Gly	Ser
														20	30

Pro	Glu	Thr	Gly	Ala	Gly	Ala	Gly	Thr	Val	Ala	Thr	Thr	Pro	Ala	Ser
														35	45

Ser	Pro	Val	Thr	Leu	Ala	Glu	Thr	Gly	Ser	Thr	Leu	Leu	Tyr	Pro	Leu
														50	60

Phe	Asn	Leu	Trp	Gly	Pro	Ala	Phe	His	Glu	Arg	Tyr	Pro	Asn	Val	Thr
														65	80

Ile	Thr	Ala	Gln	Gly	Thr	Gly	Ser	Gly	Ala	Gly	Ile	Ala	Gln	Ala	Ala
														85	95

Ala	Gly	Thr	Val	Asn	Ile	Gly	Ala	Ser	Asp	Ala	Tyr	Leu	Ser	Glu	Gly
														100	110

Asp	Met	Ala	Ala	His	Lys	Gly	Leu	Met	Asn	Ile	Ala	Leu	Ala	Ile	Ser
														115	125

Ala	Gln	Gln	Val	Asn	Tyr	Asn	Leu	Pro	Gly	Val	Ser	Glu	His	Leu	Lys

130	135	140
Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr		
145	150	155
Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro		
165	170	175
Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr		
180	185	190
Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly		
195	200	205
Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly		
210	215	220
Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu		
225	230	235
Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala		
245	250	255
Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn		
260	265	270
Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Gly Phe		
275	280	285
Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro		
290	295	300
Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn		
305	310	315
Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu		
325	330	335
His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val		
340	345	350
His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu		
355	360	365
Ile Ala Thr Ile Ser Ser		
370		

## (2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1993 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

TGTTCTTCGA	CGGCAGGCTG	GTGGAGGAAG	GGCCCACCGA	ACAGCTGTT	TCCTCGCCGA	60
AGCATGCGGA	AACCGCCCGA	TACGTCGCGG	GACTGTCGGG	GGACGTCAG	GACGCCAAGC	120
GCGGAAATTG	AAGAGCACAG	AAAGGTATGG	CGTGAAATT	CGTTGCATA	CGCTGTTGGC	180
CGTGTGACCC	GCTGCGCCCG	TGCTGCTAGC	ACCGGCGGGC	TGTGGCTCGA	AACCACCGAG	240
CGGTTGCCT	GAAACGGGCG	CCGGCGCCCG	TACTGTCGGG	ACTACCCCCG	CGTCGTCGCC	300
GGTGACGTTG	GCGGAGACCG	GTAGCACGCT	GCTCTACCCG	CTGTTCAACC	TGTGGGGTCC	360
GGCCTTTAC	GAGAGGTATC	CGAACGTAC	GATCACCGCT	CAGGGCACCG	GTTCTGGTGC	420
CGGGATCGCG	CAGGCGCCCG	CCGGGACGGT	CAACATTGGG	GCCTCCGACG	CCTATCTGTC	480
GGAAAGGTGAT	ATGGCGCGC	ACAAGGGGCT	GATGAACATC	GCGCTAGCCA	TCTCCGCTCA	540
GCAGGTCAAC	TACAACCTGC	CCGGAGTGG	CGAGCACCTC	AAGCTGAACG	GAAAAGTCCT	600
GGCGGCCATG	TACCAGGCCA	CCATCAAAC	CTGGGACGAC	CCGCAGATCG	CTGCGCTCAA	660
CCCCGGCGTG	AACTGCGCCG	GCACCGCGGT	AGTTCCGCTG	CACCGCTCCG	ACGGGTCCGG	720
TGACACCTTC	TTGTTCAACCC	AGTACCTGTC	CAAGCAAGAT	CCCGAGGGCT	GGGGCAAGTC	780
GCCCCGGCTTC	GGCACCCACCG	TCGACTTCCC	GGCGGTGCGG	GGTGCCTGG	GTGAGAACGG	840
CAACGGCGGC	ATGGTGACCG	GTTGCGCCGA	GACACGGGC	TGCGTGGCCT	ATATCGGCAT	900
CAGCTTCTC	GACCAAGGCCA	GTCAACGGGG	ACTCGCGAG	GCCCRACTAG	GCATAGCTC	960
TGGCAATTTC	TTGTTGCGCG	ACCGCGAAAG	CATTCAAGCC	GGGGCGGCTG	GCTTCGCATC	1020
GAAAACCCCG	GGGAACCAAG	CGATTTCGAT	GATGACGGG	CCCGCCCCGG	ACGGCTACCC	1080
GATCATCAAC	TACGAGTAGC	CCATCGTC	CAACCGGCCA	AAGGACGCCG	CCACCGGCCA	1140
GACCTTGCAG	GCATTTCTGC	ACTGGGCAT	CACCGACGGC	AACAAGGCCT	CGTTCCCTCGA	1200
CCAGGTTCAT	TTCCAGGCCG	TGCCGCCCCG	GGTGGTGAAG	TTGTCGACG	CGTTGATCGC	1260
GACGATTTC	AGCTAGCTC	GTTGACCACC	ACCGCACAGC	AACTCCGTC	GGGCCATCGG	1320
GCTGCTTTC	GGAGCATGCT	GGCCCGTGCC	GGTGAAGTCG	GCCGCGCTGG	CCCGGCCATC	1380
CGGTGGTTGG	GTGGGATAGG	TGCCGTCGATC	CCGCTGCTTG	CGCTGGTCTT	GGTGCCTGGT	1440
GTGCTGGTCA	TCGAGGGAT	GGGTGCGATC	AGGCTCAACG	GGTTGCATT	CTTCACCGCC	1500
ACCGAATGGA	ATCCAGGCCA	CACCTACGGC	GAAACCGTTG	TCACCGACGC	GTGCCCCATC	1560
CGGTGGCGC	CTACTACGGG	GGTGTGCCG	TGATCGTCGG	GACGCTGGCG	ACCTCGGCCA	1620

TCGCCCTGAT CATCGCGGTG CCGGTCTCTG TAGGAGCGGC GCTGGTGATC GTGGAACGGC 1680  
 TGCCGAAACG GTTGGCCGAG GCTGTGGAA TAGTCCTGGA ATTGCTCGCC GGAATCCCCA 1740  
 GCGTGGTCGT CGGTTTGTGG GGGGCAATGA CGTTCGGGCC GTTCATCGCT CATCACATCG 1800  
 CTCCGGTGAT CGCTCACAAAC GCTCCCGATG TGCCGGTGCT GAACTACTTG CGCGGCGACC 1860  
 CGGGCAACGG GGAGGGCATG TTGGTGTCCG GTCTGGTGTG GTCGGGTGATG GTCGTCCCCA 1920  
 TTATCGCCAC CACCACTCAT GACCTGTTCC GGCAGGTGCC GGTGTTGCC CGGGAGGGCG 1980  
 CGATCGGGAA TTC 1993

## (2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Met Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro  
 1 5 10 15

Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser  
 20 25 30

Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser  
 35 40 45

Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu  
 50 55 60

Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr  
 65 70 75 80

Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala  
 85 90 95

Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly  
 100 105 110

Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser  
 115 120 125

Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys  
 130 135 140

Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr  
 145 150 155 160

Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro  
 165 170 175  
 Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr  
 180 185 190  
 Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly  
 195 200 205  
 Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly  
 210 215 220  
 Ala Leu Gly Glu Asn Gly Asn Gly Met Val Thr Gly Cys Ala Glu  
 225 230 235 240  
 Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala  
 245 250 255  
 Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn  
 260 265 270  
 Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Gly Phe  
 275 280 285  
 Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro  
 290 295 300  
 Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn  
 305 310 315 320  
 Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu  
 325 330 335  
 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val  
 340 345 350  
 His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu  
 355 360 365  
 Ile Ala Thr Ile Ser Ser  
 370

## (2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1777 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GGTCTTGACC ACCACCTGGG TGTCGAAGTC GGTGCCCGGA TTGAAGTCCA GGTACTCGTG	60
GGTGGGGCGG GCGAAACAAT AGCGACAAGC ATGCGAGCAG CCGCGGGTAGC CGTTGACGGT	120

GTAGCGAAAC GGCAACGCGG CCGCGTTGGG CACCTTGTTC AGCGCTGATT TGCACAAACAC	180
CTCGTGGAAAG GTGATGCGT CGAATTGTGG CGCGCGAACG CTGCGGACCA GGCGGATCCG	240
CTGCAACCCG GCAGCGCCCG TCGTCAACCG GCATCCCGTT CACCGCGACG GCTTGCGGG	300
CCCAACGCAT ACCATTATTC GAACAACCGT TCTATACTTT GTCAACGCTG GCCGCTACCG	360
AGCGCCGCAC AGGATGTGAT ATGCCATCTC TGCGCGCACA GACAGGAGGC AGGCCTTATG	420
ACAGCATTGCG GCGTCGAGCC CTACGGGAG CCGAAGTACC TAGAAATCGC CGGGAAAGCGC	480
ATGGCGTATA TCGACGAAAGG CAAGGGTGC GCCATCGTCT TTCAGCACGG CAACCCCACG	540
TCGTCTTACT TGTGGCGCAA CATCATGGCG CACTTGGAAAG GGCTGGGCGG GCTGGTGGCC	600
TGCGATCTGA TCGGGATGGG CGCGTCGGAC AAGCTCAGCC CATCGGGACC CGACCGCTAT	660
AGCTATGGCG AGCAACGAGA CTTTTTGTTC GCGCTCTGGG ATGCGCTCGA CCTCGCGAC	720
CACGTGGTAC TGGTGCTGCA CGACTGGGGC TCGCGCTCG GCTTCGACTG GGCTAACCGAG	780
CATCGCGACC GAGTGCAGGG GATCGCGTTC ATGGAAGCGA TCGTCACCCC GATGACGTGG	840
GCGGACTGGC CGCCGGCCGT GCGGGGTGTG TTCCAGGGTT TCCGATCGCC TCAAGGGAG	900
CCAATGGCGT TGGAGCACAA CATCTTGTGCA GAACGGGTGC TGCCCGGGGC GATCCTCGA	960
CAGCTCAGCG AGGAGGAAT GAACCACTAT CGCGGCCAT TCGTGAACGG CGCGGAGGAC	1020
CGTGCCTTCA CGTTGTCGTG GCCACGAAAC CTTCCAATCG ACGGTGAGCC CGCGGAGGTC	1080
GTCGCGTGG TCAACGAGTA CGGGAGCTGG CTCGAGGAAA CGGACATGCC GAAACTGTTC	1140
ATCAACGCCG AGCCCGGCGC GATCATCACC GGCGCATCC GTGACTATGT CAGGAGCTGG	1200
CCCAACCAGA CGCAAATCAC AGTGCCCCGC GTGCATTGTC TTCAAGGAGGA CAGCGATGGC	1260
GTCGTATCGT GGGCGGGCGC TCGCGACCAT CGCGACCTG GGAGCGCTCT CATTTCACGA	1320
GACCAAGAAT GTGATTTCCG GCGAAGGGCG CGCCCTGCTT GTCAACTCAT AAGACTTCCT	1380
GCTCCGGGCA GAGATTCTCA GGAAAAGGG CACCAATCGC AGCCGCTTCC TTGCAACGA	1440
GGTCGACAAA TATACGTGGC AGGACAAAGG TCTTCCTATT TGCCAGCGA ATTAGTCGCT	1500
GCCTTTCTAT GGGCTCAGTT CGAGGAAGCC GAGCGGATCA CGCGTATCCG ATTGGACCTA	1560
TGGAACCGGT ATCATGAAAG CTTCGAATCA TTGGAACAGC GGGGGCTCCG GCGCGTCCG	1620
ATCATCCAC AGGGCTGCTC TCACAAACGCC CACATGTACT ACGTGTTACT AGCGCCACG	1680
GCGGATCGGG AGGAGGTGCT GGCAGCGTCTG ACGAGCGAAG GTATAGGCGC GGTCTTTCAT	1740

TACGTGCCGC TTCACGATTC GCCGGCCGGG CGTCGCT

1777

## (2) INFORMATION FOR SEQ ID NO:157:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GAGAGTGAAT CGTACCGGTC TCCCTAGCGG CTCCGTCCCG	TGAATGCCCA TATCACGCAC	60
GGCCCATGTTG TGGCTGTGCA CCTTCGCCCC ATGCCCGGAC	GTGGTAAAC CCAGGGTTTG	120
ATCAGTAATT CGGGGGGACG GTTGCGGGAA GGCGGCCAGG	ATGTGCGTGA GCCGC GGCGC	180
CGCCGTCGCC CAGGGCACCG CTGGATGCTC AGCCCCGGTG	CGGGCACGTA GCCAGCGTT	240
GGGGCGGTGTC GTCCACAGTG GTACTCCGGT GACGACGCCG	CGGGGTGCCT GGGTGAAAGAC	300
CGTGACCCGAC GCCGCCGATT CAGA		324

## (2) INFORMATION FOR SEQ ID NO:158:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

GCGGTACCGC CGCGTTGCGC TGGCACGGGA CCTGTACGAC	CTGAACCACT TCGCCTCGCG	60
AAAGATTGAC GAAACCGCTCG TCGGGCGGCT GTGGGTGCTC	AAGGTGTGGG GTGATGTCGT	120
CGATGACCGG CGCGGCCACCC GGCCACTAAG CGTCGAAGAC	GTCTCGCCG CCCGCAGCGA	180
GCACGACTTC CAGCCCGACT CGATCGGCGT GCTGACCCGT	CCTGTGCTA TGGCTGCCTG	240
GGAAAGCTCGC GTTGGAAAGC GATTTGCGTT CCTCACTGAC	CTCGACGCCG ACGAGCAGCG	300
GTGGGCCGCC TGGGACAAAC GGCAACGCCCG CGAAGTGGAG	AACGCGCTGG CGGTGCTCG	360
GTCCTGATCA ACCTGCCGC GATCGTGCCTG TTCCGCTGGC	ACGGTTGCGG CTGGACGCCG	420
CTGAATCGAC TAGATGAGAG CAGTTGGCA CGAACCGCCG	TGTGGTGGTG AGCAAGACAC	480
GAGTACTGTC ATCACTATTG GATGCACTGG ATGACCGGCCG	TGATTCAAGCA GGACCAATGG	540
AACTGCCCGG GGCAAAACGT CTCGGAGATG ATCGCGCTCC	CCTCGGAACC CTGCGGTGCT	600
GGCGTCAATTC GGACATCGGT CGGGCTCGCG GGATCGTGGT	GACGCCAGCG CTGAAGGAGT	660

GGAGCGCGGC	GGTGCACGCG	CTGCTGGACG	GCCGGCAGAC	GGTGCTGCTG	CGTAAGGGCG	720
GGATCGCGA	GAAGCGCTTC	GAGGTGGCGG	CCCACGAGTT	CTTGTGTTTC	CCGACGGTCG	780
CGCACAGCCA	CGCCGAGCGG	GTTCGCCCCG	AGCACCGCGA	CCTGCTGGGC	CCGGCGGCCG	840
CCGACAGCAC	CGACGAGTGT	GTGCTACTGC	GGGCCGCAGC	GAAAGTTGTT	GCCGCACTGC	900
CGGTTAACCG	GCCAGAGGGT	CTGGACGCCA	TCGAGGATCT	GCACATCTGG	ACCGCCGAGT	960
CGGTGCGCGC	CGACCGGCTC	GACTTTCGGC	CCAAGCACAA	ACTGGCCGTC	TTGGTGGTCT	1020
CGGCGATCCC	GCTGGCCGAG	CCGGTCCGGC	TGGCGCGTAG	GCCCGAGTAC	GGCGGTTGCA	1080
CCAGCTGGGT	GCAGCTGCCG	GTGACGCCGA	CGTTGGCGC	GCCGGTGAC	GACGAGGGCG	1140
CGCTGGCGGA	GGTCGCCGCC	CGGGTCCCGG	AGGCCGTGGG	TTGACTGGGC	GGCATCGCTT	1200
GGGCTCTGAGC	TGTACGCCA	GTCGGCGCTG	CGAGTGTATCT	GCTGTCGGTT	CGGTCCCTGC	1260
TGGCGTCAAT	TGACGGCGC	GGCAACAGCA	GCATTGGCGG	CGCCATCCTC	CGCGCGGCCG	1320
GCGCCCACCG	CTACAAACC					1338

## (2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

CGGGCGGCAC	CGCGGGCAC	GGCGGTACCG	GCGGCAACGG	CGCTGACGCC	GCTGCTGTGG	60
TGGGCTTCGG	CGCGAACGGC	GACCTGGCT	TCGCTGGCGG	CAAAGGCGGT	AACGGCGGAA	120
TAGGTGGGC	CGCGGTGACA	GGCGGGTTCG	CGGGCGACGG	CGGCACCGGC	GGCAAAGGTG	180
GCACCGCGG	TGCGGGCGGC	GCGGCAACAG	ACGCGCGCAG	CACCGGCAAT	CCCGGCGGTA	240
AGGGCGGCAG	CGCGGGGATC	GGCGGTGCGG	GGGGGGCGG	CGGCACGGCC	GGCACCGGCA	300
ACGGCGGCCA	TGCCGGCAAC					321

## (2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

GAAGACCCGG	CCCCGCCATA	TCGATCGGCT	CGCCGACTAC	TTTCGCGGAA	CGTGCACCGC	60						
GC	GGCGT	CGG	GCT	GATCATC	ACCGGTGGCT	ACGCGCCCAA	CCGCACCGGA	TGGCTGCTGC	120			
CG	TT	CGC	CTC	CGAAC	CTCGTC	ACTTCGGCGC	AAGCCCAGC	GCACCGCCGA	ATCACCA	180		
CG	GT	CC	ACGA	TTCGGGTGCA	AAAGATCCTGC	TGCAAATCCT	GCACGCGGAA	CGCTACG	CCT	240		
AC	CA	CC	ACT	TGCGGT	CGTCAGC	GCCTCGCGA	TCAAGGC	GATCAC	CCCCG	300		
GA	GC	CA	CTATC	GGCTCG	GGG	GTCGAAGCGA	CCATCGCGA	TTTCG	CCCCG	TGCGC	360	
TG	GG	CC	GGCG	TGCGGT	CTAC	GACGGCGT	CG	AAATCAT	GGG	CAGCGA	AGT	420
AT	CA	GG	TTCT	GGCG	CCGCGC	ACCAACAAGC	GCACCG	ACTC	GTGGGG	CGGG	ACACCG	480
AC	CG	TC	CGCCG	GT								492

## (2) INFORMATION FOR SEQ ID NO:161:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Phe	Ala	Gln	His	Leu	Val	Glu	Gly	Asp	Ala	Val	Glu	Leu	Trp	Arg	Ala
1						5				10				15	
Asn	Ala	Ala	Asp	Gln	Ala	Asp	Pro	Leu	Gln	Pro	Gly	Ser	Ala	Arg	Arg
						20			25				30		
Gln	Arg	Ala	Ser	Arg	Ser	Pro	Arg	Arg	Leu	Ala	Gly	Pro	Asn	Ala	Tyr
						35			40				45		
His	Tyr	Ser	Asn	Asn	Arg	Ser	Ile	Leu	Cys	Gln	Arg	Trp	Pro	Leu	Pro
						50			55				60		
Ser	Ala	Ala	Gln	Asp	Val	Ile	Cys	His	Leu	Cys	Pro	His	Arg	Gln	Glu
						65			70				75		80
Pro	Gly	Leu	Met	Thr	Ala	Phe	Gly	Val	Glu	Pro	Tyr	Gly	Gln	Pro	Lys
						85			90				95		
Tyr	Leu	Glu	Ile	Ala	Gly	Lys	Arg	Met	Ala	Tyr	Ile	Asp	Glu	Gly	Lys
						100			105				110		
Gly	Asp	Ala	Ile	Val	Phe	Gln	His	Gly	Asn	Pro	Thr	Ser	Ser	Tyr	Leu
						115			120				125		
Trp	Arg	Asn	Ile	Met	Pro	His	Leu	Glu	Gly	Leu	Gly	Arg	Leu	Val	Ala

130	135	140
Cys Asp Leu Ile Gly Met Gly Ala Ser Asp Lys Leu Ser Pro Ser Gly		
145	150	155
160		
Pro Asp Arg Tyr Ser Tyr Gly Glu Gln Arg Asp Phe Leu Phe Ala Leu		
165	170	175
Trp Asp Ala Leu Asp Leu Gly Asp His Val Val Leu Val His Asp		
180	185	190
Trp Gly Ser Ala Leu Gly Phe Asp Trp Ala Asn Gln His Arg Asp Arg		
195	200	205
Val Gln Gly Ile Ala Phe Met Glu Ala Ile Val Thr Pro Met Thr Trp		
210	215	220
Ala Asp Trp Pro Pro Ala Val Arg Gly Val Phe Gln Gly Phe Arg Ser		
225	230	235
240		
Pro Gln Gly Glu Pro Met Ala Leu Glu His Asn Ile Phe Val Glu Arg		
245	250	255
Val Leu Pro Gly Ala Ile Leu Arg Gln Leu Ser Asp Glu Glu Met Asn		
260	265	270
His Tyr Arg Arg Pro Phe Val Asn Gly Gly Glu Asp Arg Arg Pro Thr		
275	280	285
Leu Ser Trp Pro Arg Asn Leu Pro Ile Asp Gly Glu Pro Ala Glu Val		
290	295	300
Val Ala Leu Val Asn Glu Tyr Arg Ser Trp Leu Glu Glu Thr Asp Met		
305	310	315
320		
Pro Lys Leu Phe Ile Asn Ala Glu Pro Gly Ala Ile Ile Thr Gly Arg		
325	330	335
Ile Arg Asp Tyr Val Arg Ser Trp Pro Asn Gln Thr Glu Ile Thr Val		
340	345	350
Pro Gly Val His Phe Val Gln Glu Asp Ser Asp Gly Val Val Ser Trp		
355	360	365
Ala Gly Ala Arg Gln His Arg Arg Pro Gly Ser Ala Leu Ile Ser Arg		
370	375	380
Asp Gln Glu Cys Asp Phe Arg Arg Arg Arg Pro Ala Cys Gln Leu		
385	390	395
400		
Ile Arg Leu Pro Ala Pro Gly Arg Asp Ser Gln Gly Lys Gly His Gln		
405	410	415
Ser Gln Pro Leu Pro Ser Gln Arg Gly Arg Gln Ile Tyr Val Ala Gly		
420	425	430

Gln Arg Ser Ser Tyr Leu Pro Ser Glu Leu Val Ala Ala Phe Leu Trp  
 435 440 445  
 Ala Gln Phe Glu Glu Ala Glu Arg Ile Thr Arg Ile Arg Leu Asp Leu  
 450 455 460 "  
 Trp Asn Arg Tyr His Glu Ser Phe Glu Ser Leu Glu Gln Arg Gly Leu  
 465 470 475 480  
 Leu Arg Arg Pro Ile Ile Pro Gln Gly Cys Ser His Asn Ala His Met  
 485 490 495  
 Tyr Tyr Val Leu Leu Ala Pro Ser Ala Asp Arg Glu Glu Val Leu Ala  
 500 . 505 510  
 Arg Leu Thr Ser Glu Gly Ile Gly Ala Val Phe His Tyr Val Pro Leu  
 515 520 525  
 His Asp Ser Pro Ala Gly Arg Arg  
 530 535

## (2) INFORMATION FOR SEQ ID NO:162:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Asn Glu Ser Ala Pro Arg Ser Pro Met Leu Pro Ser Ala Arg Pro Arg  
 1 5 10 15  
 Tyr Asp Ala Ile Ala Val Leu Leu Asn Glu Met His Ala Gly His Cys  
 20 25 30  
 Asp Phe Gly Leu Val Gly Pro Ala Pro Asp Ile Val Thr Asp Ala Ala  
 35 40 45  
 Gly Asp Asp Arg Ala Gly Leu Gly Val Asp Glu Gln Phe Arg His Val  
 50 55 60  
 Gly Phe Leu Glu Pro Ala Pro Val Leu Val Asp Gln Arg Asp Asp Leu  
 65 70 75 80  
 Gly Gly Leu Thr Val Asp Trp Lys Val Ser Trp Pro Arg Gln Arg Gly  
 85 90 95  
 Ala Thr Val Leu Ala Ala Val His Glu Trp Pro Pro Ile Val Val His  
 100 105 110  
 Phe Leu Val Ala Glu Leu Ser Gln Asp Arg Pro Gly Gln His Pro Phe  
 115 120 125

10081813 022502

Asp Lys Asp Val Val Leu Gln Arg His Trp Leu Ala Leu Arg Arg Ser  
 130 135 140  
 Glu Thr Leu Glu His Thr Pro His Gly Arg Arg Pro Val Arg Pro Arg  
 145 150 155 160  
 His Arg Gly Asp Asp Arg Phe His Glu Arg Asp Pro Leu His Ser Val  
 165 170 175  
 Ala Met Leu Val Ser Pro Val Glu Ala Glu Arg Arg Ala Pro Val Val  
 180 185 190  
 Gln His Gln Tyr His Val Val Ala Glu Val Glu Arg Ile Pro Glu Arg  
 195 200 205  
 Glu Gln Lys Val Ser Leu Leu Ala Ile Ala Ile Ala Val Gly Ser Arg  
 210 215 220  
 Trp Ala Glu Leu Val Arg Arg Ala His Pro Asp Gln Ile Ala Gly His  
 225 230 235 240  
 Gln Pro Ala Gln Pro Phe Gln Val Arg His Asp Val Ala Pro Gln Val  
 245 250 255  
 Arg Arg Arg Gly Val Ala Val Leu Lys Asp Asp Gly Val Thr Leu Ala  
 260 265 270  
 Phe Val Asp Ile Arg His Ala Leu Pro Gly Asp Phe  
 275 280

## (2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 264 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

ATGAACATGT CGTCGGTGGT GGGTCGCAAG GCCTTTCGCG GATTGCGCGG CTACTCCTCC	60
GCCATGCACG CGATCGCCGG TTTCTCCGAT GCGTTGCGCC AAGAGCTGCG GGGTAGCGGA	120
ATCGCCGTCT CGGTGATCCA CCCGGCGCTG ACCCAGACAC CGCTGTTGGC CAACGTCGAC	180
CCCGCCGACA TGCCGCCGCC GTTTCGCGAGC CTCACGCCCA TTCCCGTTCA CTGGGTGCG	240
GCAGCGGTGC TTGACGGTGT GGC	264

## (2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1171 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

TAGTCGGCGA	CGATGACGTC	GCGGTCCAGG	CCGACCGCTT	CAAGCACCAAG	CGCGACCAAG	60
AAGCCGGTGC	GATCCTTAC	CGCGAACGAG	TGGGTGAGCA	CCGGGCGTCC	GGCGGCAAGC	120
AGTGTGACGA	CACGATGTAG	CGCGCGCTGT	GCTCCATTGC	GGCTTGGAA	TTGGCGATAC	180
TCGTCGGTCA	TGTAGCGGGT	GGCCGCGTCA	TTTATCGACT	GGCTGGATTC	GCCGGACTCG	240
CCGTTGGACC	CGTCATTGGT	TAGCAGCCTC	TTGAATGCGG	TTTCGTGCGG	CGCTGAGTCG	300
TCGGCGTCAT	CATCGGGCAG	GTCGGGGAAC	GGCAGCAGGT	GGACGTCGAT	GCCGTCCGGA	360
ACCCGTCCTG	GACCGCGCGC	GGCAACCTCC	CGGGACGACC	GCAGGTCGGC	AACGTCGGTG	420
ATCCCCGACG	GGCGCAGCGT	TGCCCCCTCGT	GCCGAAATTG	GCACGAGGCT	GGCGAGGCCAC	480
CGGGCATCAC	CAAGCAACGC	TTGCCCAAGTA	CGGATCGTCA	CTTCCGCATC	CGGCAGACCA	540
ATCTCCTCGC	CGCCCATCGT	CAGATCCCGC	TCGTGCGITG	ACAAGAACGG	CGCGAGATGT	600
GCCAGGGGT	ATCGGAGATT	GAACCGCGCA	CCGAGTTCTT	CAATCGTGC	GCGCTGCCGC	660
ACTATTGGCA	CTTTCCGGCG	GTCGCGGTAT	TCAGCAAGCA	TGCGAGTCTC	GACGAACTCG	720
CCCCACGTA	CCCACGGCGT	AGCTCCGGC	GTGACGCGGA	GGATCGGGG	GTGATCTTG	780
CCGACACGCT	CGTAGCCGTT	GATCCACCGC	TTCGCGGTG	CGGGGGGAG	GCCGATCAGC	840
TTATCGACCT	CGGC GTATGC	CGACGGCAAG	CTGGGCGCGT	TCGTCGAGGT	CAAGAACCTCC	900
ACCATCGGCA	CCGGCACCAA	GGTGCCGCAC	CTGACCTACG	TCGGCGACGC	CGACATCGGC	960
GAGTACAGCA	ACATCGCGC	CTCCAGCGT	TTCGTCAACT	ACGACGGTAC	GTCCAAACGG	1020
CGCACCAACG	TGGTTCGCA	CGTACGGACC	GGGTCCGACA	CCATGTTCGT	GGCCCCAGTA	1080
ACCATCGCGC	ACGGCGCGTA	TACCGGGGCC	GGCACAGTGG	TGCGGGAGGA	TGTCCCGCCG	1140
GGGGCGCTGG	CAGTGTGCGG	GGGTCCCGCAA	C			1171

## (2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 227 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GC	AAAGGCGG	CACCGGGGG	GCCGGCATGA	ACAGCCTCGA	CCCCTGCTA	GCCGCCAAG	60
AC	GGCGGCCA	AGGCGGCACC	GGCGGCACCG	GCGGCAACGC	CGGCGCCGCG	GGCACCCAGCT	120
TC	ACCCAAAGG	CGCCGACGGC	AACGCCGGCA	ACGGCGGTGA	CGGCGGGGTC	GGCGGCCAACG	180
GC	GGAAACGG	CGGAAACGGC	GCAGACAACA	CCACCACCGC	CGCCGCC		227

## (2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

CCTCGCCACC	ATGGGCAGGC	AGGGCGGTAG	CGGTGGCGCC	GGCTCTACCC	CAGGCGCAA	60
GGGC	GGCC	GGCTTCACTC	CAACCAAGCG	CGGCGACGGC	GGCGACGGCG	120
CAAC	CTCC	CAA	GTGGTCGGCG	GCAACGGCG	CGACGGCGC	180
CGCC	GGCG	GGCG	GGCGCAACG	GGCGCGCGG	CGGCGACGGC	240
CAAC	GCC	GGC	AACCCTGGTG	AAACGGGCC	AAACGGTAAC	300
CGGC						304

## (2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GTGGGACGCT	GCCGAGGCTG	TATAACAAGG	ACAACATCGA	CCAGCGCCGG	CTCGGTGAGC	60
TGATCGACCT	ATTTAACAGT	GCGCGCTTCA	GCGGGCAGGG	CGAGCACCGC	GCCCCGGATC	120
TGATGGGTGA	GGTCTACGAA	TACTTCCTCG	GCAATTTCGC	TCGCGCGGAA	GGGAAGCGGG	180
GTGGCGAGTT	CTTTACCCCG	CCCAGCGTGG	TCAAGGTGAT	CGTGGAGGTG	CTGGAGCCGT	240
CGAGTGGCG	GGTGTATGAC	CCGTGCTGCG	GTTCCGGAGG	CATGTTGTG	CAGACCGAGA	300
AGTTCATCTA	CGAACACGAC	GGCGATCCGA	AGGATGTCTC	GATCTATGGC	CAGGAAAGCA	360
TTGAGGAGAC	CTGGCGGATG	GCAGAGATGA	ACCTCGCCAT	CCACGGCAGC	GACAACAAGG	420

GGCTCGGC	CCGATGGAGT	GATACTTCG	CCCGCGACCA	GCACCCGGAC	GTGCAGATGG	480
ACTACGTGAT	GGCCAATCG	CCGTTCAACA	TCAAAGACTG	GGCCCGCAAC	GAGGAAGACC	540
CACGCTGGCG	CTTCGGTGT	CCGCCCCGCA	ATAACGCCA	CTACGCATGG	ATTCAGCACA	600
TCCGTACAA	CTTGGCGCCG	GGAGGTCGGG	CGGGCGTGGT	GATGGCCAAC	GGTCGATGT	660
CGTCGAAC	CAACGCCAAG	GGGGATATTC	CGCGCAAAT	CGTGGAGGGC	GATTTGGTTT	720
CCTGCATGGT	CGCGTTACCC	ACCCAGCTGT	TCCGCAGCAC	CGGAATCCCG	GTGTGCCTGT	780
GGTTTTTCG	CAAAAACAAAG	CGGGCAGGTA	AGCAAGGGTC	TATCAACCGG	TGCGGGCAGG	840
TGCTGCTCAT	CGACGCTCGT	GAACGGGGC	ACCTAGTGG	CGGGGCCGAG	CGGGCGCTGA	900
CCAACAGAGGA	GATCGTCCGC	ATCGGGATA	CCTTCCACGC	GAGCACGACC	ACCGGCAACG	960
CCGGCTCCGG	TGGTGC	GGTAATGGGG	GCACGGCCT	CAACGGCGCG	GGCGGTGCTG	1020
GGGGGCCCGG	CGGCAACCGG	GGTGTGCGG	GGGTGTCCTT	CGGCAACGCT	GTGGGCGGGC	1080
ACGGCGGCAA	CGGCGGCAAC	GGCGGCCACG	CGCGCGACGG	CACGACGGGC	GGCGCCGGGC	1140
GCAAGGGCGG	CAACGGCAGC	AGCGGTGCGG	CCAGCGGCTC	AGGCCTCGTC	AACGTACCG	1200
CCGGCCACGG	CGGCAACGGC	GGCAATGGCG	GAACGGGG	CAACGGCTCC	GGGGCGCCCG	1260
GGGGCCAGGG	CGGTGC	GGCAGCGCGG	GAACGGGG	CAACGGCGC	GGTGCCACCG	1320
GGGGCGCCAG	CGGCAAGGGC	GGCAACGGCA	CCAGCGGTGC	CGGCAGCGGC	TCAGGCGTCA	1380
TCAACGTCA	CGCCGGCCAC	GGCGCAACG	GGGGCAATGG	CGGCAACGGC	GGCAACGGC	1439

## (2) INFORMATION FOR SEQ ID NO:168:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GGCCGGCGG	GGCCGGATT	TETCGTGCCT	TGATTGTGCG	TGGGGATAAC	GGCGGTGATG	60
GTGGTAA	CGGGATGGGC	GGGGCTGGCG	GGGCTGGCGG	CCCCGGCGGG	GCCGGCGGCC	120
TGATCAGCCT	GCTGGGCGGC	CAAGGGCGCG	GGGGGGCGGG	CGGGACCGGC	GGGGCCGGCG	180
GTGTTGGCGG	TGACGGGGG	GGCGGCGGCC	CGGGCAACCA	GGCCTTCAC	GCAGGTGCGG	240
GGGGGGCGG	CGGCCTGATC	AGCCTGCTGG	GGGGCAAGG	GGGGGGCGGG	GCCGGCGGGG	300
CGGGCGGGGC	CGGCGGTGTT	GGCGGTGAC				329

## (2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GCAACGGTGG CAACGGCGGC ACCAGCACGA CGGTGGGAT GGCGGGAGGT AACTGTGGTG	60
CCGCCGGGCT GATCGGCAAC	80

## (2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

GGGCTGTGTC GCACTCACAC CGCCGCATTC GGCGACGTTG GCCGCCAAT ATCCAGCTCA	60
AGGCCTACTA CTTACCGTCG GAGGACGCC GCATCAAGGT GCGGGTCAGC GCCCAAGGAA	120
TCAAGGTCAT CGACCGCGAC GGGCATCGAG GCCGTCGTCG CGCGGCTCGG GCAGGGATCCG	180
CCCCGGCGCA CTTCGCGCGC CAAGCGGGCT CATCGCTCCG AACGGCGGCG ATCCTGTGAG	240
CACAAGTGT GGCACGCAAC GAGATTGTC CAAATTGTCAA GCCGTGTTCG ACCGCAGGGA	300
CCGGTTATAC GTATGTCAAC CTATGTCACT CGCAAGAACCC GGCAAAACGA TCCCCGTGATC	360
CGCCGACAGC CCACGAGTGC AAGACCGTTA CA	392

## (2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

ACCGGGCGCCA CGGGCGGCAC CGGGTTCGCC GGTGGCGCCG GCGGGGCCGG CGGGCAGGGC	60
GGTATCAGCG GTGCCGGCGG CACCAACGGC TCTGGTGGCG CTGGCGGCAC CGGGCGACAA	120
GGCGGGCCCG GGGGCGCTGG CGGGGCCGGC GCCGATAACC CCACCGGCAT CGGCGCGGCC	180

GGCGGCACCG	GGGGCACCGG	CGGAGCGGCC	GGAGCCGGCG	GGGCCGGTGG	CGCCATCGGT	240
ACCGGGGGCA	CGGGCGGCCG	GGTGGGGCAGC	GTCTGGTAACG	CCGGGATCGG	CGGTACCGGC	300
GGTACGGGTG	GTGTCGGTGG	TGCTGGTGGT	GCAGGTGCGG	CTGCGGCCGC	TGGCAGCAGC	360
GCTACCGGTG	GGCGCGGGTT	CGCCGGCCGC	GCCGGCGGAG	AAGGCGGACC	GGGCGGCAAC	420
AGCGGTGTGG	GGGGCACCAA	CGGCTCCGGC	GGCAGCCGGC	GTGAGCGGG	CAAGGGCGGC	480
ACCGGAGGTG	CGGGCGGGTCA	CGGCGCGGAC	AACCCACCG	GTGCTGGTTT	CGCCG	535

## (2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

CCGACGTGCG	CGGGGCGATA	CGGGGGTCAC	CGACTACTAC	ATCATCCGCA	CCGAGAATCG	60
GCCGCTGCTG	CAACCGCTGC	GGGCGGTGCG	GGTCATCGGA	GATCCGCTGG	CCGACCTGAT	120
CCAGCCGAAC	CTGAAGGTGA	TGTCAAACCT	GGGCTACCGC	GACCCGAACT	ACGGCTACTC	180
GACGAGCTAC	GCCGATGTGC	GAACGCCGTT	CGGGCTGTGG	CCGAACTGTC	CGCCTCAGGT	240
CATCGCCGAT	GCCCTGGCCG	CGGAAACACA	AGAAGGCATC	CTTGACTTCA	CGGGCCGACCT	300
GCAGGGCTG	TCCGGCAAC	CGCTCACGCT	CCCGCAGATC	CAGCTGCCGC	AACCCGCCGA	360
TCTGGTGGCC	GGCGGTGGCCG	CCGCACCGAC	GCCGGCCGAG	GTGGTGAACA	CGCTCGCCAG	420
GATCATCTCA	ACCAAACCTACG	CCGTCCTGTCT	GCCCACCGTG	GACATGCC	TCGGCTGGTC	480
ACCACCCCTGC	CCGTGTACAC	CACCCACACTG	TTCGTCAGGC	AACTCGCTGC	GGGCAATCTG	540
ATCAACCCGA	TGGCTATCC	CCTGGCGGCC	ACCGTAGGTT	TAGGCACGAT	CGATAGCGGG	600
CGGCCTGGAA	TTGCTCACCC	TCCTCGGCC	GGCCTCGAC	ACCGTTCGAA	ACATCGAGGG	660
CCTCGTACCA	TAACGGATTC	CCGACGGCAT				690

## (2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

ACGGTGACGG CGGTACTGGC GCGGCCACG GCGGCAACGG CGGGAATCCC GGGTGGCTCT	60
TGGGCACAGC CGGGGGTGGC GGCAACGGTG GCGCCGGCAG CACCGGTACT GCAGGTGGCG	120
GCTCTGGGGG CACCGGGCGC GACGGCGGGA CCGGCGGGCG TGCGGGCTG TTAATGGGCG	180
CCGGCGCCGG CGGGCACGGT GGCACGTGGCG GCGCGGGCGG TGCGGGTGTG GACGGTGGCG	240
GCGCCGGCGG GGCGCGGGG GCGCGGGCGA ACGGCGGCAC CGGGGTCAA GCGCCCTGC	300
TGTTCGGGCG CGCGGGCACCC GCGGAGGCCG CGGGCTACGG CGCGATGGC GGTGGCGCG	360
GTGACGGCTT CGACGGCACG ATGGCGGCCG TGGGTGGTAC CGGTGGC	407

## (2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GATCGGTCA CGCATCCCCC TCGCGGCCAA GCGATTCCGC GGTCTCACCG AAGAACATCG	60
TGCACGCGGC GGCGCGGACC AGCCCGCTGC GCTGCGGC GTCGAACGCC TCCAGCAGGC	120
ACAGCCAGTC CTTGGCGGCC TGCGAGGCCA ACACGTCGGT GTCACCGGTG TAGATCGCCG	180
GGATGCCCGC CTCCGCCAAC GCATTCGGC ACGCCCGCGC GTCTTGTGA TGCTCGACGA	240
TCACCGCGAT GTCTGCGGCC ACCACGGGCC GCCCGGCCAA GGTGGCCCG CTGGCCAGTA	300
GCGCCGCGAC GTCGGCGGCC AGGTCGTCGG GGATGTGCCG GCGCAGCGCT CCGGCGCGAC	360
GCCCCAAAAA CGACCCCTCA CCCAGCTGGG TCCCGCTGGC ATATCCCTTG CCGTCCTGGG	420
CGATATTGGA CGCGCATGCC CGCACCGCGT ACAGGCCGCC CACCACCG	468

## (2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GGTGGTAAACG GCGGCCAGGG TGGCATCGGC GCGGCCGGCG AGAGAGGCCG CGACGGCGCC	60
GGCCCCAATG CTAACGGCGC AACAGGCCAG AACGGCGGTAA GCGGTGGTAA CGGTGGCGAC	120

GGCGGGCGCCG GCGGCAATGG CGGCGCGGGC GGCAACGCGC AGGCGGCCGG GTACACCGAC	180
GGCGCCACGG GCACCGCCGG CGACGGCGGC AACGGCGGC	219

## (2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

TAGCTCCGGC GAGGGCGGCA AGGGCGCGA CGGTGGCCAC GCGGGTGAAC GCGTCGGCGG	60
CAACAGTTCC GTCACCCAAG GCGGCAGCGG CGGTGGCGGC GGCGCCGGCG GCGCCGGCGG	120
CAGCGGCTTT TTCGGCGGCA AGGGCGGCTT CGCGGGCGAC GGCGGTCAAG GCGGCCCGGAA	180
CGGGCGGCGT ACCGTCGGCA CGCTGGCCGG TGCGCGCGC AACGGCGGTG TCGGCGGCCG	240
GGCGGGCGAC GGCGTCTTTG CGCGTGGCGG CGGCCAGGGC GGCTCGGTG GGCAGGGCGG	300
CAATGGCGGC GGCTCCACCG GCGCAACCG CGGCCCTGGC GGCGCGGGCG GTGGCGGAGG	360
CAACGCCCGC GCTCGTGGCG AATCCGGGCT GACCATGGAC AGCGCGGCCA AGTTCGCTGC	420
CATCGCATCA GGCGCGTACT GCCCGAACAT CCTGGAACAT CACCCGAGTT AGCGGGGCCG	480
ATTTCTGTAT CACC	494

## (2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GGGCCGGTGG TGCGCGGGC CAGCTCTTCA GCGCCGGAGG CGCGGCGGGT GCGTTGGGG	60
TTGGCGGCAC CGGGGGCAG GGTGGGGCTG GCGGTGCGCG AGCGGCCGGC GCCGACGCC	120
CCGCCAGCAC AGGTCTAACCG GGTGGTACCG GGTCGCTGG CGGGGCCGGC GGCGTCGGCG	180
GCCAGAGCGG CAACGCCATT GCCGGCGGC A TCAACGGCTC	220

## (2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

ATGGCGGCCAA CGGGGGCCCC GGCGGTGCTG GCGGGGCCGG CGACTACAAAT TTCCAACGGC	60
GGGCAGGGTG GTGCCGGCGG CCAAGGCCGC CAAGGCCGCC TGCGGGGGC AAGCACCAC	120
TGATCGGCCT AGCCGCACCC GGGAAAGCCG ATCCAACAGG CGACGATGCC GCCTTCCTTG	180
CCCGCGTTGGA CCAGGCCGGC ATCACCTACG CTGACCCAGG CCACGCCATA ACGGCCGCCA	240
AGGCAGATGTG TGGGCTGTGT GCTAACGGCG TAACAGGTCT ACAGCTGGTC GCGGACCTTG	300
GGGACTACAA TCCCGGGCTG ACCATGGACA GCGCGGCCAA GTTCGCTGCC ATCGCATCAG	360
GGCGTACTG CCCCCAACAC CTGGAACA	388

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GCAAAGCGG CACCGGGGGG GCCGGCATGA ACAGCCTCGA CCCGCTGCTA GCCGCCAAG	60
ACGGCGGCCA AGGCGGCACC GGCGGCACCG GCGGCAACGC CGGGCCCGGC GGCACCAAGT	120
TCACCCAAAG CGCCGACGGC AACGCGGCAC ACGGCGGTGA CGGGGGGTC GGCGGCCAAG	180
GCGGAAACGG CGGAAACGGC GCAGACAACA CCACCAACGC CGCCGCCGGC ACCACAGGC	240
GCGACGGCGG GGCGGGCGGG GCGGGCGGAA CGGGCGGAAC CGGGCGAGCC GCCGGCACCG	300
GCACCGCGG CCAACAAAGGC AACGGCGGCAC ACGGCGGCAC CGGGGGAAA GGCGGCACCG	360
GGCGCGACGG TGCACCTCTCA GGCAGCACCG GTGGTGCCGG	400

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 538 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GGCAACGGCG GCAACGGCGG CATGCCGGC ATTGGGCGGC AACGGCGTTC CGGGACGGGC	60
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AGCGGCAACG GCGGCCAACG GCGGCAGCGG CGGCAACGGC GGCAACGCCG GCATGGGGG	120
CAACAGCGGC ACCGGCAGCG GCGACGGCGG TGCCGGGGG AACGGCGGG CGGCGGGCAC	180
GGGCGGCACC GGCGGCACG GCGGCCTCAC CGGTACTGGC GGCACCGCG GCAGCGGTGG	240
CACCGGGCTG GACGGCGGTA ACGGCGGCAA CGGAGCAGAT AACACCGCAA ACATGACTGC	300
GCAGGGGGC GGTGACGGTG GCACCGCGG CGACGGTGGC TTCGGCGGGC GGGCGGGGGC	360
CGGCGGGCTG GGCTTGACCG CTGGCGCCAA CGGCACCGGC GGGCAAGGCG GCGCCGGGG	420
CGATGGGGC AACGGGGGCA TCGGCGGCCA CGGCCCACTC ACTGACGACC CGGGCGGCAA	480
CGGGGGCACCG GCGGCCAACG GCGGCACCGG CGGCACCGGC GGCGGGGCCA TCGGCGAC	538

## (2) INFORMATION FOR SEQ ID NO:181:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

GGGCGGGTGG TGCCGGGGC CAGCTCTTCA GGGCGGGAGG CGCGCGGGT GCCGTTGGGG	60
TTGGCGGCAC CGGCGGCCAG GGTGGGGCTG GCGGTGCCGG AGCGGCCGGC GCCGACGCC	120
CCGCAGCAC AGGTCTAACCG GGTGGTACCG GGTTCGCTGG CGGGGCCGGC GGCGTCGGCG	180
GCCACGGCGG CAACGCCATT GCGGGGGCA TCAACGGCTC CGGTGGTGCC GGCGGCAC	239

## (2) INFORMATION FOR SEQ ID NO:182:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 985 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

AGCAGGCCATA CCGGTGGCGC CGGGTTGGCC GCGGGCGGGC GCGGAGAAGG CGGAGCGGGC	60
GGCAACAGCG GTGTGGCGG CACCAACGGC TCCGGCGCGC CGGGCGGTGC AGGCGGCAG	120
GGCGGCACCG GAGGTGGCGG CGGGTCCGGC GCGGACAACC CCACCGGTGC TGGTTTCGCC	180
GGTGGCCCG GCGGCACAGG TGCGGGGGC GCGGGCGGG GGGCGGGGG GGCGACCGGT	240
ACCGGGCGCA CGGGCGCGGT TGTCGGCGCC ACCGGTAGTG CAGGCATCGG CGGGCGGGC	300
GGCGCGGGCG GTGACGGCGG CGATGGGGCC AGCGGTCTCG GCCTGGGCT CTCCGGCTTT	360

GACGGCGGCC AAGGCGGCCA AGGCGGGGCC GGCGGCAGCG CGGGCGCCGG CGGCATCAAC 420  
 GGGGCGCGCG GGGCGCGCGG CAACGGCGGC GACGGCGGGG ACGGCGCAAC CGGTGCGCGA 480  
 GGTCTCGCGC ACAACGGCGG GGTCGGCGGT GACGGTGGGG CGGGTGGCGC CGCCGGCAAC 540  
 GGCGGCAACG CGGGCGTCGG CCTGACAGCC AAGGCGGGCG ACGGCGGGCGC CGCGGGCAAT 600  
 GCGCGCAACG GGGCGCGCGG CGGTGCTGGC GGGGCGGGCG ACAACAATT CAACGGCGC 660  
 CAGGGTGGTG CGGGCGGCCA AGGCGGCCA GGCGGCTGG GCGGGGCAAG CACCACTGA 720  
 TCGGCCTAGC CGCACCCGGG AAAGCCGATC CAACAGCGA CGATGCCGCC TTCCCTGCCG 780  
 CGTTGGACCA GGCGGCATC ACCTACGCTG ACCCAGGCCA CGCCATAACG GCCGCCAAGG 840  
 CGATGTGTGG GCTGTGTGCT AACGGCGTAA CAGGTCTACA GCTGGTCGCG GACCTGCGG 900  
 AATAACAATCC CGGGCTGACC ATGGACAGCG CGGCCAAGTT CGCTGCCATC GCATCAGGCC 960  
 CGTACTGCC CGAACACCTG GAACA 985

## (2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

CGGCACGAGG ATCGGTACCC CGCGGCATCG GCAGCTGCCG ATTGCGCCGGG TTTCCCCACCC 60  
 CGAGGAAAGC CGCTTACCAAGA TGGCGCTGCCA GAAGTAGGGC GATCCGTTCG CGATGCCGGC 120  
 ATGAACGGGC GGCATCAAAT TAGTGCAGGA ACCTTTCACT TTAGCGACGA TAATGGCTAT 180  
 AGCACTAAGG AGGATGATCC GATATGACGC AGTCGACGAC CGTGCACGGTG GATCAGCAAG 240  
 AGATTTGAA CAGGGCAAC GAGGTGGAGG CCCCAGATGGC GGACCCACCG ACTGATGTCC 300  
 CCATCACACC GTGCGAACCTC ACGGCGGCCA AAAACGCCGC CCAACAGCTG GTATTGTCCG 360  
 CCGACACACAT CGGGGAATAC CTGGCGGCCG GTGCCAAAGA CGGGCAGCGT CTGGCGACCT 420  
 CGCTGCGCAA CGCGGCCAAG GCGTATGCCG AGGTTGATGA GGAGGCTGCC ACCCGCGCTGG 480  
 ACAACGACGG CGAAGGAACG GTGCAGGCAG AATCGGCCGG GGCGCTGCCA GGGGACAGTT 540  
 CGGCGAACT AACCGATACT CGCAGGGTGG CCACGGCCGG TGAACCCAAC TTCATGGATC 600  
 TCAAAGAAGC GGCAAGGAAG CTCGAAACCGG GCGACCAAGG CGCATCGCTC GCGCACTTTG 660

CGGATGGGTG GAACACTTTC AACCTGACGC TGCAAGGCAG CGTCAAGCGG TTCCGGGGT 720  
 TTGACAACCTG GGAAGGGAT GCGGCTACCG CTTGCGAGGC TTCGCTCGAT CAACAAACGGC 780  
 AATGGATACT CCACATGGCC AAATTGAGCG CTGCGATGGC CAAGCAGGCT CAATATGTGCG 840  
 CGCAGCTGCA CGTGTGGGCT AGGCAGGAAC ATCCGACTTA TGAAGACATA GTCGGGCTCG 900  
 AACGGCTTAA CGCGGAAAC CCTTCGGCCCC GCGACCAAAT TCTCCGGGTG TACGGGGAGT 960  
 ATCAGCAGAG GTCCGAGAAG GTGCTGACCG AATACAACAA CAAGGCAGCC CTGGAAACGG 1020  
 TAAACCCGCC GAAGCCTCCC CCCGCCATCA AGATCGACCC GCCCCCGCCT CCGCAAGAGC 1080  
 AGGGATTGAT CCCCTGGCTTC CTGATGCCCG CGTCTGACGG CTCCGGTGTG ACTCCGGTA 1140  
 CCGGGATGCC AGCCGCACCG ATGGTTCGGC CTACCGGATC GCGGGGTGGT GGCCTCCCG 1200  
 CTGACACGGC GGCGCAGCTG ACCTGCGCTG GGCGGGAAAGC CGCAGCGCTG TCAGGGCAGC 1260  
 TGGCGGTCAA AGCGGCATCG CTCGGTGGCG GTGGAGGCCG CGGGGTGCGC TCGGGCCCGT 1320  
 TGGGATCCGC GATCGGGGCC GCCGAATCGG TGCGGCCCGC TGGCGCTGGT GACATTGCCG 1380  
 GCTTAGGCCA GGGAGGGCC GGCGCGGCCG CGCGCCTGGG CGCGGGTGGC ATGGGAATGCG 1440  
 CGATGGGTGC CGCGCAGTCAG GGACAAGGGG GCGCCAAGTC CAAGGGTTCT CAGCAGGAAG 1500  
 ACGAGGGCCT CTACACCGAG GATCGGGCAT GGACCGAGGC CGTCATTGGT AACCGTCGGC 1560  
 GCCAGGACAG TAAGGAGTCG AAGTGAACAT GGACGAATTG GACCCGCATG TCGCCCGGGC 1620  
 GTTGACGCTG CGGGCCGGT TTCAGTCGGC CCTAGACGGG ACGCTCAATC AGATGAACAA 1680  
 CGGATCCTTC CGCGCACCAG ACGAAGCCGA GACCGTCGAA GTGACGATCA ATGGGCACCA 1740  
 GTGGCTCACCG GGCCTGCCA TCGAAGATGG TTTGCTGAAG AAGCTGGGTG CCGAGGGCGT 1800  
 GGCTCAGCGG GTCAACGAGG CGCTGCACAA TGCGCAGGCC GCGGGCTCCG CGTATAACCA 1860  
 CGCGGGGGC GAGCAGCTGA CCGCTGCCGT ATCGGCCATG TCCCGGCCGA TGAACGAAGG 1920  
 AATGGCTAA GCCCATTGTT GCGGTGGTAG CGACTACGCA CCGAATGAGC GCGCAGATGC 1980  
 GGTCAATTCA CGCGCCCCAC ACGGCGTGAG TACGCATTGT CAATGTTTG ACATGGATCG 2040  
 GCGGGTTCG GAGGGCGCCA TAGTCCTGGT CGCCAATATT GCGCGACGCTA GCTGGTCTTA 2100  
 GGTTGGTTA CGCTGGTTAA TTATGACGTC CGTACCA 2138

## (2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Met Thr Gln Ser Gln Thr Val Thr Val Asp Gln Gln Glu Ile Leu Asn  
 1 5 10 15

Arg Ala Asn Glu Val Glu Ala Pro Met Ala Asp Pro Pro Thr Asp Val  
 20 25 30

Pro Ile Thr Pro Cys Glu Leu Thr Ala Ala Lys Asn Ala Ala Gln Gln  
 35 40 45

Leu Val Leu Ser Ala Asp Asn Met Arg Glu Tyr Leu Ala Ala Gly Ala  
 50 55 60

Lys Glu Arg Gln Arg Leu Ala Thr Ser Leu Arg Asn Ala Ala Lys Ala  
 65 70 75 80

Tyr Gly Glu Val Asp Glu Glu Ala Ala Thr Ala Leu Asp Asn Asp Gly  
 85 90 95

Glu Gly Thr Val Gln Ala Glu Ser Ala Gly Ala Val Gly Gly Asp Ser  
 100 105 110

Ser Ala Glu Leu Thr Asp Thr Pro Arg Val Ala Thr Ala Gly Glu Pro  
 115 120 125

Asn Phe Met Asp Leu Lys Glu Ala Ala Arg Lys Leu Glu Thr Gly Asp  
 130 135 140

Gln Gly Ala Ser Leu Ala His Phe Ala Asp Gly Trp Asn Thr Phe Asn  
 145 150 155 160

Leu Thr Leu Gln Gly Asp Val Lys Arg Phe Arg Gly Phe Asp Asn Trp  
 165 170 175

Glu Gly Asp Ala Ala Thr Ala Cys Glu Ala Ser Leu Asp Gln Gln Arg  
 180 185 190

Gln Trp Ile Leu His Met Ala Lys Leu Ser Ala Ala Met Ala Lys Gln  
 195 200 205

Ala Gln Tyr Val Ala Gln Leu His Val Trp Ala Arg Arg Glu His Pro  
 210 215 220

Thr Tyr Glu Asp Ile Val Gly Leu Glu Arg Leu Tyr Ala Glu Asn Pro  
 225 230 235 240

Ser Ala Arg Asp Gln Ile Leu Pro Val Tyr Ala Glu Tyr Gln Gln Arg  
 245 250 255

Ser Glu Lys Val Leu Thr Glu Tyr Asn Asn Lys Ala Ala Leu Glu Pro  
 260 265 270

Val Asn Pro Pro Lys Pro Pro Pro Ala Ile Lys Ile Asp Pro Pro Pro  
 275 280 285  
 Pro Pro Gln Glu Gln Gly Leu Ile Pro Gly Phe Leu Met Pro Pro Ser  
 290 295 300 ~  
 Asp Gly Ser Gly Val Thr Pro Gly Thr Gly Met Pro Ala Ala Pro Met  
 305 310 315 320  
 Val Pro Pro Thr Gly Ser Pro Gly Gly Leu Pro Ala Asp Thr Ala  
 325 330 335  
 Ala Gln Leu Thr Ser Ala Gly Arg Glu Ala Ala Ala Leu Ser Gly Asp  
 340 345 350  
 Val Ala Val Lys Ala Ala Ser Leu Gly Gly Gly Gly Gly Gly Val  
 355 360 365  
 Pro Ser Ala Pro Leu Gly Ser Ala Ile Gly Gly Ala Glu Ser Val Arg  
 370 375 380  
 Pro Ala Gly Ala Gly Asp Ile Ala Gly Leu Gly Gln Gly Arg Ala Gly  
 385 390 395 400  
 Gly Gly Ala Ala Leu Gly Gly Gly Met Gly Met Pro Met Gly Ala  
 405 410 415  
 Ala His Gln Gly Gln Gly Ala Lys Ser Lys Gly Ser Gln Gln Glu  
 420 425 430  
 Asp Glu Ala Leu Tyr Thr Glu Asp Arg Ala Trp Thr Glu Ala Val Ile  
 435 440 445  
 Gly Asn Arg Arg Arg Gln Asp Ser Lys Glu Ser Lys  
 450 455 460

## (2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Ala Gly Asn Val Thr Ser Ala Ser Gly Pro His Arg Phe Gly Ala Pro  
 1 5 10 15  
 Asp Arg Gly Ser Gln Arg Arg Arg His Pro Ala Ala Ser Thr Ala  
 20 25 30  
 Thr Glu Arg Cys Arg Phe Asp Arg His Val Ala Arg Gln Arg Cys Gly  
 35 40 45

205320-E1848001

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Arg	Val	Ala	Ala	Ser	Phe	Ile	Asp	Trp	Leu	Asp	Ser	Pro	Asp	Ser	Pro
1					5				10						15
Leu Asp Pro Ser Leu Val Ser Ser Leu Leu Asn Ala Val Ser Cys Gly															
					20				25			"		30	
Ala Glu Ser Ser Ala Ser Ser Ser Ala Arg Ser Gly Asn Gly Ser Arg															
					35				40				45		
Trp Thr Ser Met Pro Ser Gly Thr Arg Pro Gly Pro Arg Arg Ala Thr															
					50				55				60		
Ser Arg Asp Asp Arg Arg Ser Ala Thr Ser Val Ile Pro Ser Arg Arg															
					65				70				75		80
Ser Val Ala Pro Arg Ala Glu Phe Gly Thr Arg Leu Ala Ser His Arg															
					85				90				95		
Ala Ser Pro Ser Asn Ala Cys Pro Val Arg Ile Val Thr Ser Ala Ser															
					100				105				110		
Gly Arg Pro Ile Ser Ser Pro Pro Ile Val Arg Ser Arg Ser Cys Val															
					115				120				125		
Asp Lys Asn Gly Arg Arg Cys Ala Ser Gly Tyr Arg Arg Leu Asn Arg															
					130				135				140		
Ala Arg Ser Ser Ser Ile Ala Ala Arg Cys Arg Thr Ile Gly Thr Phe															
					145				150				155		160
Arg Arg Ser Arg Tyr Ser Ala Ser Met Arg Val Ser Thr Asn Ser Pro															
					165				170				175		
His Val Thr His Gly Val Ala Pro Gly Val Thr Arg Arg Ile Gly Gly															
					180				185				190		

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Gln Glu Arg Pro Gln Met Cys Gln Arg Val Ser Glu Ile Glu Pro Arg  
 1 5 10 15  
 Thr Gln Phe Phe Asn Arg Cys Ala Leu Pro His Tyr Trp His Phe Pro  
 20 25 30  
 Ala Val Ala Val Phe Ser Lys His Ala Ser Leu Asp Glu Leu Ala Pro

35                    40                    45

Arg Asn Pro Arg Arg Ser Ser Arg Arg Asp Ala Glu Asp Arg Arg Val  
50 55 60

Ile Phe Ala Ala Thr Leu Val Ala Val Asp Pro Pro Leu Arg Gly Ala  
65 70 75 80

Gly Gly Glu Ala Asp Gln Leu Ile Asp Leu Gly Val Cys Arg Arg Gln  
 85 90 95

Ala Gly Arg Val Arg Arg Gly Gln Glu Leu His His Arg His Arg His  
100 105 110

Gln Gly Ala Ala Pro Asp Leu Arg Arg Arg Arg Arg His Arg Arg Val  
115 120 125

Gln Gln His Arg Arg Leu Gln Arg Val Arg Gln Leu Arg Arg Tyr Val  
130 135 140

Gln Thr Ala His His Arg Arg Phe Ala Arg Thr Asp Arg Val Arg His  
145 150 155 160

His Val Arg Gly Pro Ser Asn His Arg Arg Arg Arg Val Tyr Arg Gly  
165 170 175

Arg His Ser Gly Ala Gly Gly Cys Pro Ala Gly Gly Ala Gly Ser Val  
180 185 190

Gly Gly Ser Ala  
195

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Val Arg Cys Gly Thr Leu Val Pro Val Pro Met Val Glu Phe Leu Thr  
1 5 10 15

Ser Thr Asn Ala Pro Ser Leu Pro Ser Ala Tyr Ala Glu Val Asp Lys  
20 25 30

Leu Ile Gly Leu Pro Ala Gly Thr Ala Lys Arg Trp Ile Asn Gly Tyr  
35 40 45

Glu Arg Gly Gly Lys Asp His Pro Pro Ile Leu Arg Val Thr Pro Gly  
50 55 60

Ala Thr Pro Trp Val Thr Trp Gly Glu Phe Val Glu Thr Arg Met Leu

65	70	75	80
Ala Glu Tyr Arg Asp Arg Arg Lys Val Pro Ile Val Arg Gln Arg Ala			
85		90	95
Ala Ile Glu Glu Leu Arg Ala Arg Phe Asn Leu Arg Tyr Pro Leu Ala			
100		105	110
His Leu Arg Pro Phe Leu Ser Thr His Glu Arg Asp Leu Thr Met Gly			
115	120		125
Gly Glu Glu Ile Gly Leu Pro Asp Ala Glu Val Thr Ile Arg Thr Gly			
130	135		140
Gln Ala Leu Leu Gly Asp Ala Arg Trp Leu Ala Ser Leu Val Pro Asn			
145	150	155	160
Ser Ala Arg Gly Ala Thr Leu Arg Arg Leu Gly Ile Thr Asp Val Ala			
165	170		175
Asp Leu Arg Ser Ser Arg Glu Val Ala Arg Arg Gly Pro Gly Arg Val			
180	185		190
Pro Asp Gly Ile Asp Val His Leu Leu Pro Phe Pro Asp Leu Ala Asp			
195	200		205
Asp Asp Ala Asp Asp Ser Ala Pro His Glu Thr Ala Phe Lys Arg Leu			
210	215		220
Leu Thr Asn Asp Gly Ser Asn Gly Glu Ser Gly Glu Ser Ser Gln Ser			
225	230	235	240
Ile Asn Asp Ala Ala Thr Arg Tyr Met Thr Asp Glu Tyr Arg Gln Phe			
245	250		255
Pro Thr Arg Asn Gly Ala Gln Arg Ala Leu His Arg Val Val Thr Leu			
260	265		270
Leu Ala Ala Gly Arg Pro Val Leu Thr His Cys Phe Ala Gly Lys Asp			
275	280		285
Arg Thr Gly Phe Val Val Ala Leu Val Leu Glu Ala Val Gly Leu Asp			
290	295		300
Arg Asp Val Ile Val Ala Asp			
305	310		

## (2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2072 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

CTCGTGCAGA	TTCGGCACGA	GCTGAGCAGC	CCAAGGGGCC	GTTCGGCGAA	GTCATCGAGG	60
CATTGCGCGA	CGGGCTGGCC	GGCAAGGGTA	AGCAAATCAA	CACCAACGCTG	AACAGCCTGT	120
CGCAGGGCGTT	GAACGCTTGTG	AATGAGGGCC	CGGGCGACTT	CTTCGCGGTG	GTACGCGAGC	180
TGGCCTATT	CGTCAACCGG	CTACATCAGG	ACGACCAAACA	GTTCGTCGCG	TTGAACAAGA	240
ACCTTGCGGA	GTTCACCGAC	AGGTTGACCC	ACTCCGATGC	GGACCTGTGCG	AACGCCATCC	300
AGCAATTGCA	CAGCTTGCTC	GCCGTCGCGC	GCCCGTTCTT	CGCCAAGAAC	CGCGAGGTGC	360
TGACGCATGA	CGTCAATAAT	CTCGCGACCG	TGACCACCAAC	GTTCGTCGAG	CCCGATCCGT	420
TGGATGGTT	GGAGACCGTC	CTGCACATCT	TCCCGACGCT	GGCGGCGAAC	ATTAACCGAC	480
TTTACCATCC	GACACACCGT	GGCGTGGTGT	CGCTTTCCCG	GTTCACGAAT	TTCGCCAACC	540
CGATGGAGTT	CATCTGCGC	TCGATTCAAG	CGGGTAGCCG	GTTCGGTTAT	CAAGAGTCGG	600
CCGAACCTCTG	TGCGCAGTAT	CTGGCGCCAG	TCCTCGATGC	GATCAAGTT	AACTACTTT	660
CGTTCGGCCT	GAACGTGGCC	AGCACCGCCT	CGACACTGCC	TAAGAGATC	CGCTACTCCG	720
AGCCCCGCTT	GCAGCCGCC	AACGGGTACA	AGGACACCAAC	GGTGCCTGGC	ATCTGGGTGCG	780
CGGATACGCC	GTGTCACAC	CGAACACCGC	AGCCCGTTG	GGTGGTGGCA	CCCGGGATGC	840
AAGGGGTTCA	GGTGGGACCG	ATCACGCGAG	GTTCGCTGAC	GCCGGAGTCC	CTGGCCGAAC	900
TCATGGGTGG	TCCCGATATC	GCCCCCTCGT	CGTCAGGGCT	GCAAAACCCCG	CCCGGACCCCG	960
CGAATGCGTA	CGACGAGTAC	CCCGTGCCTGC	CGCCGATCGG	TTTACAGGCC	CCACAGGTGC	1020
CGATACCAACC	GCCGCTCTCT	GGGCCGAGC	TAATCCCCTG	TCCGGTGCA	CCGGTCTTGG	1080
CGGCATCGT	GTTCCCAAGA	GATGCCCGG	CAGCGTCGGA	AAACTTCGAC	TACATGGGCC	1140
TCTTGTGCT	GTGCGCGGGC	CTGGCGACCT	TCCTGTTGG	GGTGTGATCT	AGCCCCGCC	1200
GTGGAACGAT	GGCCGATCGG	CACGTGTTGA	TACCGGCGAT	CACCGGCC	CGCTTGATCG	1260
CGGCATTCTG	CGCACATTG	TGGTACCGCA	CAGAACATCC	GCTCATAGAC	ATGCGCTTGT	1320
TCCAGAACCG	AGCGGTCGCG	CAGGCCAAC	TGACGATGAC	GGTGTCTCC	CTCGGGCTGT	1380
TTGGCTCTT	CTTGCTGCTC	CCGAGCTACC	TCCAGCAAGT	GTTCGACCAA	TCACCGATGC	1440
ATCGGGGGT	GCATATCATC	CCACAGGCC	TCGGTGCAT	GCTGGCGATG	CCGATCGCCG	1500
GAGCGATGAT	GGACCGACCG	GGACCGGCCA	AGATCGTGT	GGTTGGGATC	ATGCTGATCG	1560
CTGCGGGGTT	GGGCACCTTC	GCCTTGGTG	TCGCGCGCA	AGCGGACTAC	TTACCCATT	1620

TGCCGACCGG GCTGGCAATC ATGGGCATGG GCATGGGCTG CTCCATGATG CCACTGTCCG	1680
GGGCGGCAGT GCAGACCTCG GCCCCACATC AGATCGCTCG CGGTCGACG CTGATCGCG	1740
TCAACCAGCA GGTGGGCGGT TCGATAGGGA CCGCACTGAT GTCCGGTGCCT CTCACCTACC	1800
AGTTCAATCA CAGCGAAATC ATCGCTACTG CAAAGAAAGT CGCACTGACC CCAGAGAGTG	1860
GCGCCGGCG GGGGGCGCG GTTGACCCCTT CCTCGCTACC GCGCCAAACC AACTTCGCG	1920
CCCAACTGCT GCATGACCTT TCGCACGCCCT ACGCGGTGGT ATTCTGTGATA GCGACCGCGC	1980
TAGTGGTCTC GACGCTGATC CCCGCGGCAT TCCTGCCGAA ACAGCAGGCT AGTCATCGAA	2040
GAGCACCGTT GCTATCCGCA TGACGTCTGC TT	2072

## (2) INFORMATION FOR SEQ ID NO:190:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1923 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

TCACCCCCGA GAACTCGTTC GTCGACGACC TGGACATCGA CTCGCTGTG ATGGTCGAGA	60
TCGCCGTGCA GACCGAGGAC AAGTACGGCG TCAAGATCCC CGACGAGGAC CTGCGGGTC	120
TGCGTACCGT CGGTGACGTT GTCCGCTACA TCCAGAAAGCT CGAGGAAGAA AACCCGGAGG	180
CGGCTCAGGC GTTGCAGCGC AAGATTGAGT CGGAGAACCC CGATGCGGCA CGAGCAGATC	240
GGTGCAGTTTC ACCCACATCG CAAGCTCGAG ACGCCCGTGC TCCTCTTGCA CGCTCAGCCA	300
GGTTGGCGTG TCGCCGCCTT CCAGCAAGTG TTCCCACACAC AGAAGGGAC CCTCGCGAAA	360
GGTGACTGAT CGCGCGACCA CATACTCGAT GCCACCGTGG CTGACAATTG CGCGGGTCC	420
GAGTTGGCGG GGGCCGAATT GCGGCATTGC GTCGAAGGCC AGCGGATCCC GGCGCCCGCC	480
CGGCCTGGCT GGTGTTTTGG GCCGCGGAT GGCCACGACG AGAACGACGA TGGCGGGAT	540
GAACAGCGCC ACGGCAATCA CGACCAGCAG ATTCACCGC CATACTCTT CGTACCGCTG	600
CGCCGCGGTT GGTGCGATCG TCGCATATCG ATGGCGCCGT TTAACGTAAC AGCTTTGCG	660
GGACCGGGGG TCACAAACGGG CGAGTTGTC GGCGGGAAC CGGGCAGGTC TCGGCCGCGG	720
TCACCCCCAGC TCACTGGTGC ACCATCCGGG TGTCGGTGAAG CGTGCACACTC AAACACACTC	780
AACGGCAACG GTTTCTCAGG TCACCAAGCTC AACCTCGACC CGCAATCGCT CGTACGTTTC	840

GACCGCGCGC AGGTCGCGAG TCAGCAGCTT TCGGCCGGCA GCTTCGCCG TGAAGCCGAC 900  
 CAGGGCATCG TAGGTTGCGC CACCGGTGAC ATCGTGTCTG GCGAGGTGGT CGGTCAAGCC 960  
 GCGATATGAG CAGGCATCCA GTGCCAGGTA GTTGCTGGAG GTGATGTCCG CCAAGTAGGC 1020  
 GTGGACGCCA ACAGGGCAA TACGATGCGG CGGTGGTAGC CGGGTCAAGA CGGAATAGGT 1080  
 TTCCACAGCC GCGTGGCGCA TCAGATGGAC GCCACGGTTG AGCGCCGCA CGGGCGCCCTC 1140  
 GTGCCCTTCG TGCCAGGTCG CGAATCCGGC AACCAAGCAGC CTGGTGTCTG GTGCGATCAC 1200  
 CGCCGTGTCG GATCGAGCGT TTCCCGAACG ATTTCTGTCG TCAACGGGGG CAGGGGACGT 1260  
 TCTGGCGTG CGACGAGAAC CGAGCCTTCC CGAACCGAGTT CGACACCCGT CGGGGCCGGC 1320  
 TCAATCTCGA TGCGCCCATC GCGCTCGGTG ATCTCCACCT GGTCGTTCCC GCGCAAGCCA 1380  
 AGGCAGCTCGC GAATCCGCTT GGGATCACC AGACGTCTCG CGACATCGAT GGTTGTTCCG 1440  
 ATGGTAGGAA ATTTACCATC GCACGTTCCA TAGGGCTGTC CTGGCGGGGA TGTGGGACG 1500  
 ATCCGCTAGC GTATCGAACG ATTGTTTCGG AAATGGCTGA GGGAGCGTGC GGTGCGGGTG 1560  
 ATGGGTGTCG ATCCCGGGTT GACCCGATGC GGGCTGTCG TCATCGAGAG TGGGCGTGGT 1620  
 CGGCAGCTCA CGCGCTGGA TGTCGACGTG GTGCCACAC CGTCGATGC GGCTTGCG 1680  
 CAGCGCTGTG TGCCCATCAG CGATGCCGTC GAGCACTGGC TGGACACCCA TCATCCGGAG 1740  
 GTGGTGGCTA TCGAACGGGT GTTCTCTCAG CTCAACGTGA CCACGGTGAT GGGCACCGCG 1800  
 CAGGGCGCGC GCGTGTGTCG CCTGGGGGGC GCCAACCGTG GTGTCGACGT GCATTCAT 1860  
 ACCCCCAGCG AGGTCAAGGC GGCGGTCACT GGCAACGGTT CGCGACACAA GGTCAGGTC 1920  
 ACC 1923

## (2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1055 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

CTGGCGTGCC AGTGTCAACCG GCGATATGAC GTCGGCATTC AATTCGCGG CCCCGCCGG 60  
 CCCGTCGCCA CCCAATCTGG ACCACCCGGT CGCTCAATTG CGGAAGGTGC CCAAGTGCCT 120  
 GCCCAATGTG GTGCTGGGGT TCTTGAACGA AGGCCTGCCG TATCGGGTGC CCTACCCCCA 180  
 AACAAACGCCA GTCCAGGAAT CGGGTCCCGC GCGGCCGATT CCCAGCGCA TCTGCTAGCC 240

GGGGATGGTT CAGACGTAAC GGTTGGCTAG GTCGAAACCC GGCCAGGGC CGCTGGACGG 300  
 GCTCATGGCA GCGAAATTAG AAAACCCGGG ATATTGTCGG CGGATTGTCA TACGATGCTG 360  
 AGTGCTTGGT GGTTCGTGTGTT TAGCCATTGA GTGTGGATGT GTTGAGACCC TGGCCTGGAA 420  
 GGGGACAACG TGCTTTGCC TCTTGGTCCG CCTTTGCCGC CCGACGCCGT GGTGGCGAAA 480  
 CGGGCTGAGT CGGGAATGCT CGGGGGTTG TCGGGTCCGC TCAGCTGGGG AGTGGCTGTG 540  
 CCACCCGATG ATTATGACCA CTGGCGCCT GCGCCGGAGG ACGGCGCCGA TGTCGATGTC 600  
 CAGGCGGCCG AAGGGGCCGA CGCAGAGGCC GCGGCCATGG ACGAGTGGGA TGAGTGGCAG 660  
 GCGTGGAAACG AGTGGGTGGC GGAGAACGCT GAACCCCGCT TTGAGGTGCC ACGGAGTAGC 720  
 AGCAGCGTGA TTCCGCATTC TCCGGCGGCC GGCTAGGAGA GGGGGCGCAG ACTGTCGTTA 780  
 TTGACCAGT GATCGGCCGT CTCGGTGTTC CGCGGCCGG CTATGACAAC AGTCATAATGTG 840  
 CATGACAAGT TACAGGTATT AGGTCACGGT TCAACAAGGA GACAGGAAC ATGGCAACAC 900  
 GTTTTATGAC GGATCCGCAC GCGATGCCGG ACATGGCGGG CCGTTTGAG GTGCACGCC 960  
 AGACGGTGGA GGACGAGGCT CGCCGGATGT GGGCGTCCGC GCACAAACATC TCGGGNGCGG 1020  
 GCTGGAGTGG CATGGCCGAG GCGACCTCGC TAGAC 1055

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

CGCGCTCGTT GTTGGCATAC TCCGGCGCGG CGGCCCTGAC CGCACTGGCC GTGGCGTGTG 60  
 TCCGGGCTGA CCACCGGGAT CGCCGAACCA TCCGAGATCA CCTCGCAATG ATCCACCTCG 120  
 CGCAGCTGGT CACCCAGCCA CGGGCGGGTG TGCGACAGCG CCTGCATCAC CTTGGTATAG 180  
 CGCTCGGCC CGAGCGCAG GAAGTTGTAG TACTGGCCA CCACCTGGTT ACCGGGACGG 240  
 GAGAAGTCA GGGTGAAGGT CGGCATGTCG CCGCCGAGGT AGTTGACCCG GAAAACAGA 300  
 TCCTCCGGCA GGTGCTCGGG CCCGCGCCAC ACGACAAACC CGACGCCGGG ATAGGTCA 359

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

AACGGGCCCC	TGGGCACCGC	TCCTCTAAAGG	GCTCTCGTTG	GTCGCATGAA	GTGCTGGAAG	60
GATGCATCTT	GGCAGATTCC	CGCCAGAGCA	AAACAGCCGC	TAGTCCTAGT	CCGAGTCGCC	120
CGCAAAGTTT	CTCGAATAAC	TCCGTACCCG	GAGCGCCAAA	CCGGGTCTCC	TTCGCTAACG	180
TGCGCGAAC	ACTTGAGGTT	CCGGGACTCC	TTGACGTCCA	GACCGATTG	TTCGAGTGGC	240
TGATCGGTT	GGCGCGCTGG	CGCGAATCCG	CCGCCGAGCG	GGGTGATGTC	AACCCAGTGG	300
GTGGCCTGGA	AGAGGGCTGC	TACGAGCTGT	CTCCGATCGA	GGACTTCTCC		350

## (2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 679 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Glu	Gln	Pro	Lys	Gly	Pro	Phe	Gly	Glu	Ile	Glu	Ala	Phe	Ala	Asp	
1					5				10				15		
Gly	Leu	Ala	Gly	Lys	Gly	Lys	Gln	Ile	Asn	Thr	Thr	Leu	Asn	Ser	Leu
						20			25			30			
Ser	Gln	Ala	Leu	Asn	Ala	Leu	Asn	Glu	Gly	Arg	Gly	Asp	Phe	Phe	Ala
	35						40			45					
Val	Val	Arg	Ser	Leu	Ala	Leu	Phe	Val	Asn	Ala	Leu	His	Gln	Asp	Asp
	50						55			60					
Gln	Gln	Phe	Val	Ala	Leu	Asn	Lys	Asn	Leu	Ala	Glu	Phe	Thr	Asp	Arg
	65						70			75			80		
Leu	Thr	His	Ser	Asp	Ala	Asp	Leu	Ser	Asn	Ala	Ile	Gln	Gln	Phe	Asp
							85			90			95		
Ser	Leu	Leu	Ala	Val	Ala	Arg	Pro	Phe	Ala	Lys	Asn	Arg	Glu	Val	
	100							105			110				
Leu	Thr	His	Asp	Val	Asn	Asn	Leu	Ala	Thr	Val	Thr	Thr	Leu	Leu	
	115							120			125				
Gln	Pro	Asp	Pro	Leu	Asp	Gly	Leu	Glu	Thr	Val	Leu	His	Ile	Phe	Pro
	130						135				140				

Thr Leu Ala Ala Asn Ile Asn Gln Leu Tyr His Pro Thr His Gly Gly  
 145 150 155 160  
 Val Val Ser Leu Ser Ala Phe Thr Asn Phe Ala Asn Pro Met Glu Phe  
 165 170 175  
 Ile Cys Ser Ser Ile Gln Ala Gly Ser Arg Leu Gly Tyr Gln Glu Ser  
 180 185 190  
 Ala Glu Leu Cys Ala Gln Tyr Leu Ala Pro Val Leu Asp Ala Ile Lys  
 195 200 205  
 Phe Asn Tyr Phe Pro Phe Gly Leu Asn Val Ala Ser Thr Ala Ser Thr  
 210 215 220  
 Leu Pro Lys Glu Ile Ala Tyr Ser Glu Pro Arg Leu Gln Pro Pro Asn  
 225 230 235 240  
 Gly Tyr Lys Asp Thr Thr Val Pro Gly Ile Trp Val Pro Asp Thr Pro  
 245 250 255  
 Leu Ser His Arg Asn Thr Gln Pro Gly Trp Val Val Ala Pro Gly Met  
 260 265 270  
 Gln Gly Val Gln Val Gly Pro Ile Thr Gln Gly Leu Leu Thr Pro Glu  
 275 280 285  
 Ser Leu Ala Glu Leu Met Gly Gly Pro Asp Ile Ala Pro Pro Ser Ser  
 290 295 300  
 Gly Leu Gln Thr Pro Pro Gly Pro Pro Asn Ala Tyr Asp Glu Tyr Pro  
 305 310 315 320  
 Val Leu Pro Pro Ile Gly Leu Gln Ala Pro Gln Val Pro Ile Pro Pro  
 325 330 335  
 Pro Pro Pro Gly Pro Asp Val Ile Pro Gly Pro Val Pro Pro Val Leu  
 340 345 350  
 Ala Ala Ile Val Phe Pro Arg Asp Arg Pro Ala Ala Ser Glu Asn Phe  
 355 360 365  
 Asp Tyr Met Gly Leu Leu Leu Ser Pro Gly Leu Ala Thr Phe Leu  
 370 375 380  
 Phe Gly Val Ser Ser Pro Ala Arg Gly Thr Met Ala Asp Arg His  
 385 390 395 400  
 Val Leu Ile Pro Ala Ile Thr Gly Leu Ala Leu Ile Ala Ala Phe Val  
 405 410 415  
 Ala His Ser Trp Tyr Arg Thr Glu His Pro Leu Ile Asp Met Arg Leu  
 420 425 430  
 Phe Gln Asn Arg Ala Val Ala Gln Ala Asn Met Thr Met Thr Val Leu

435

440

445

Ser Leu Gly Leu Phe Gly Ser Phe Leu Leu Leu Pro Ser Tyr Leu Gln  
 450 455 460

Gln Val Leu His Gln Ser Pro Met Gln Ser Gly Val His Ile Ile Pro  
 465 470 475 480

Gln Gly Leu Gly Ala Met Leu Ala Met Pro Ile Ala Gly Ala Met Met  
 485 490 495

Asp Arg Arg Gly Pro Ala Lys Ile Val Leu Val Gly Ile Met Leu Ile  
 500 505 510

Ala Ala Gly Leu Gly Thr Phe Ala Phe Gly Val Ala Arg Gln Ala Asp  
 515 520 525

Tyr Leu Pro Ile Leu Pro Thr Gly Leu Ala Ile Met Gly Met Gly Met  
 530 535 540

Gly Cys Ser Met Met Pro Leu Ser Gly Ala Ala Val Gln Thr Leu Ala  
 545 550 555 560

Pro His Gln Ile Ala Arg Gly Ser Thr Leu Ile Ser Val Asn Gln Gln  
 565 570 575

Val Gly Gly Ser Ile Gly Thr Ala Leu Met Ser Val Leu Leu Thr Tyr  
 580 585 590

Gln Phe Asn His Ser Glu Ile Ile Ala Thr Ala Lys Lys Val Ala Leu  
 595 600 605

Thr Pro Glu Ser Gly Ala Gly Arg Gly Ala Ala Val Asp Pro Ser Ser  
 610 615 620

Leu Pro Arg Gln Thr Asn Phe Ala Ala Gln Leu Leu His Asp Leu Ser  
 625 630 635 640

His Ala Tyr Ala Val Val Phe Val Ile Ala Thr Ala Leu Val Val Ser  
 645 650 655

Thr Leu Ile Pro Ala Ala Phe Leu Pro Lys Gln Gln Ala Ser His Arg  
 660 665 670

Arg Ala Pro Leu Leu Ser Ala  
 675

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 120 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Thr Pro Glu Lys Ser Phe Val Asp Asp Leu Asp Ile Asp Ser Leu Ser  
 1 5 10 15  
 Met Val Glu Ile Ala Val Gln Thr Glu Asp Lys Tyr Gly Val Lys Ile  
 20 25 30  
 Pro Asp Glu Asp Leu Ala Gly Leu Arg Thr Val Gly Asp Val Val Ala  
 35 40 45  
 Tyr Ile Gln Lys Leu Glu Glu Asn Pro Glu Ala Ala Gln Ala Leu  
 50 55 60  
 Arg Ala Lys Ile Glu Ser Glu Asn Pro Asp Ala Ala Arg Ala Asp Arg  
 65 70 75 80  
 Cys Val Ser Pro Thr Ser Gln Ala Arg Asp Ala Arg Arg Pro Leu Ala  
 85 90 95  
 Arg Ser Ala Arg Leu Ala Cys Arg Arg Leu Pro Ala Ser Val Pro Thr  
 100 105 110  
 Thr Arg Arg Asp Pro Arg Glu Arg  
 115 120

## (2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 89 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Leu Ala Cys Gln Cys His Arg Arg Tyr Asp Val Gly Ile Gln Phe Arg  
 1 5 10 15  
 Gly Pro Ala Gly Pro Val Ala Thr Gln Ser Gly Pro Pro Gly Pro Ser  
 20 25 30  
 Ile Ala Glu Gly Arg Gln Val Arg Ala Gln Cys Gly Ala Gly Phe Leu  
 35 40 45  
 Glu Arg Arg Pro Ala Val Ser Gly Ala Leu Pro Pro Asn Asn Ala Ser  
 50 55 60  
 Pro Gly Ile Arg Ser Arg Ala Ala Asp Ser Gln Arg His Leu Leu Ala  
 65 70 75 80  
 Gly Asp Gly Ser Asp Val Thr Val Gly  
 85

## (2) INFORMATION FOR SEQ ID NO:197:

205220-Exhibit8001

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Ala Ser Leu Leu Ala Tyr Ser Ala Ala Ala Ala Ser Thr Ala Leu Ala  
 1 5 10 15

Val Ala Cys Val Arg Ala Asp His Arg Asp Arg Arg Arg Thr Ile Arg Asp  
 20 25 30

His Leu Ala Met Ile His Leu Ala Gln Leu Val Thr Gln Pro Pro Gly  
 35 40 45

Gly Val Arg Gln Arg Leu His His Leu Gly Ile Ala Val Ala Pro Gln  
 50 55 60

Pro Gln Glu Val Val Val Leu Ala His His Leu Val Thr Gly Thr Gly  
 65 70 75 80

Glu Val Gln Gly Glu Gly Arg His Val Ala Ala Glu Val Val Asp Pro  
 85 90 95

Glu Asn Gln Ile Leu Arg Gln Val Leu Gly Pro Ala Pro His Asp Lys  
 100 105 110

Pro Asp Ala Gly Ile Gly Gln  
 115

## (2) INFORMATION FOR SEQ ID NO:198:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Arg Ala Arg Gly His Arg Ser Ser Lys Gly Ser Arg Trp Ser His Glu  
 1 5 10 15

Val Leu Glu Gly Cys Ile Leu Ala Asp Ser Arg Gln Ser Lys Thr Ala  
 20 25 30

Ala Ser Pro Ser Pro Ser Arg Pro Gln Ser Ser Ser Asn Asn Ser Val  
 35 40 45

Pro Gly Ala Pro Asn Arg Val Ser Phe Ala Lys Leu Arg Glu Pro Leu  
 50 55 60

Glu Val Pro Gly Leu Leu Asp Val Gln Thr Asp Ser Phe Glu Trp Leu  
 65 70 75 80

Ile Gly Ser Pro Arg Trp Arg Glu Ser Ala Ala Glu Arg Gly Asp Val  
 85 90 95

Asn Pro Val Gly Gly Leu Glu Glu Val Leu Tyr Glu Leu Ser Pro Ile  
 100 105 110

Glu Asp Phe Ser  
 115

## (2) INFORMATION FOR SEQ ID NO:199:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

TGCTACGCAG	CAATCGCTTT	GGTGACAGAT	GTGGATGCGG	CGCTCGCTGC	TGGCGATGGC	60
GTGAAAGCCG	CCGACGTGTT	CGCCGCATTC	GGGGAGAACAA	TCGAACTGCT	CAAAGGCTG	120
GTGCGGGCCG	CCATCGATCG	GGTCGCCAC	GAGGGCACGT	GCACGCACGT	TCAACACCAAC	180
GCCGGTGTTC	CGTTGCCGTT	CGAGCTGCCA	TGAGGGTGCT	GCTGACCGGC	GCGGCCGGCT	240
TCATCGGTC	CGCGCTGGAT	CGCCGTTAC	GGGCTGCGGG	TCACGACGTG	GTGGGCGTGC	300
ACCGCGTGTCT	GCCCCGCCG	CACGGCCAA	ACCCGGTGCT	GCCACCGGGC	TGCCAGCGGG	360
TCGACGTGCG	CGACGCCAGC	CGCCTGGCCC	CGTTGTTGCG	CGGTGTCGAT	CTGGTGTGTC	420
ACCAGGCCGC	CATGGTGGGT	GCCGGCGTCA	ACGCCGCCGA	CGCACCCGCC	TATGGCGGCC	480
ACAACGATTT	CGCCACCAACG	GTGCTGCTGG	CGCAGATGTT	CGCCGCCGGG	GTCCGCCGTT	540
TGGTGTGGC	GTGCGTCGATG	GTGGTTACG	GGCAGGGCG	CTATGACTGT	CCCCAGCATG	600
GACCGGTGCA	CCCGCTGCCG	CGGCGGCCAG	CCGACCTGGA	CAATGGGGTC	TTGAGACACC	660
GTTGCCCGGG	GTGCGGCCAG	CCAGTCATCT	GGCAATTGGT	CGACGAGAT	GCCCCGTTGC	720
GCCCCGCCAG	CCTGTACGCG	GCAGCAAGAC	CGGCCAGGAG	CACTACGCC	TGGCGTGGTC	780
GGAAACGAAT	GGCGGTTCCG	TGGTGGCGTT	G			811

## (2) INFORMATION FOR SEQ ID NO:200:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

GTCCCGCGAT GTGGCCGAGC ATGACTTTCG GCAACACCGG CGTAGTAGTC GAAGATATCG	60
GACTTTGTGG TCCCGGTGGC GGGATAGAGC ACCTGTCGGC GTTGGTCAGC GTCACCCGTT	120
GCTCGGACGC CGAACCCATG CTTTCAACGT AGCCTGTCGG TCACACAAAGT CGCGAGCGTA	180
ACGTCACCGT CAAATATCGC GTGGAATTTC GCCGTGACGT TCCGCTCGCG GACAATCAAG	240
GCATACTCAC TTACATGCGA GCCATTTGGA CGGGTTCGAT CGCCTTCGGG CTGGTGAACG	300
TGCCGGTCAA GGTGTACAGC GCTACCGCAG ACCACGACAT CAGGGTCCAC CAGGGTGCACG	360
CCAAGGACAA CGGACGCAATC CGGTACAAGC GCGTCTGCGA GGCGTGTGGC GAGGTGGTCG	420
ACTACCGCGA TCTTGCCCCG GCCTACGAGT CCGGCGACGG CCAAATGGTG GCGATCACCG	480
ACGACGACAT CGCCAGCTTG CCTGARGAAC GCAGCCGGGA GATCGAGGTG TTGGAGTTCG	540
TCCCCGGCGC CGACGTGGAC CCGATGATGT TCGACCGCAG CTACTTTTG GAGCCTGATT	600
CGAAGTCGTC GAAATCGTAT GTGCTGCTGG CTAAGACACT CGCCGAGACC GACCGGATGG	660
CGATCGTGA TCGCCCCACC GGCGTGAAT GCAGGAAAAA TAAGAGCCGC TATCCACAT	720
TCGGCGTCGA GCTCGGCTAC CACAAACGGT AGAACGATCG AGACATTCCC GAGCTGAAGT	780
GCGGCGCTAT AGAAGCCGCT CTGCGCGATT ATCAAACGCA AAATACGCTT ACTCATGCCA	840
TCGGCGCTGC TCACCCGATG CGACGTTTTT GCCACGCTCC ACCGCTGCC GCGCGACCTC	900
AAAGTGGGCAT GCATCCCACC CGTTCCCGGA AACCGGTTCC GGCGGGTCGG CTCATCGCTT	960
CATCCT	966

## (2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2367 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

CCGCACCGCC GGCAATAACCG CCAGCGCCAC CGTTACCGCC GTTTGCGCCG TTGCCCCCGT	60
TGCCGCCCCGT CCCGCCGCC CGCGCGATGG AGTTCTCATC GCAAAGTA CTGGCGTTGC	120
CACCGGAGCC GCCGTTGCCG CGGTCACCGC CAGCCCCGCC GACTCCACCG GCCCCACCGA	180

CTCCGCCGCT	GCCACCGTTG	CCGCCGTTGC	CGATCAACAT	GCCGCTGGCG	CCACCCCTTGC	240
CACCCACGCC	ACCGGCTCCG	CCCACCCCCG	CGACACCAAG	CGAGCTGCG	CCGGAGCCAC	300
CATCACCACC	TACGCCACCG	ACCGCCAGA	CACCAGCGAC	CGGGTCTTCG	TGAAACGTCG	360
CGGTGCCACC	ACCGCCGCCG	TTACCGCCAA	CCCCACCGC	AACGCCGGC	CCGCCATCCC	420
CGCCGGCCCC	GGCCTTGCCG	CGCTTGCCGC	CGTTGCCGAA	CAACAAACCG	CCGGCGCCGC	480
CGTTGCCGCC	CGGCCGCCCG	GTCCCCGCCG	CGCCGCCGAC	GCCAAGGCCG	CTGCCGCCCT	540
TGCCGCCATC	ACCACCCCTG	CGCCGACCA	CATCGGGTTC	TGCCCTCGGG	TCTGGGCTGT	600
CAAACCTCG	GATGCCACCG	TTGCCGCCG	TTCCCCCGGG	CCCCCCCGTG	GCGCCGTCAC	660
CACCGATACC	ACCCGCCCA	CCGGCGCCAC	CGTTGCCGCC	ATCACCGAAT	AGCAACCCGC	720
CGGGGCCACC	ATTGCCGCA	GCTCCCCCTG	CGCCACCGTC	GGGCCGGAG	GCGGCACTG	780
CAGCCCCGTT	ACCACCGAAA	CCGCCGCTAC	CACCGGTAGA	GGTGGCAGTG	GCGATGTGTA	840
CGAAAGCGCC	GCCTCCGGCG	CCGGCGCTAC	CACCCCCACT	GCCGGCGGG	ACACCGTCGG	900
ACCCGTTGCC	ACCATCACCG	CCAAAAGGCGC	TCGCAATGTC	GCCCTGCGCG	ACTCCGCCGT	960
CGGGCCGCGT	GCCGCCGCCG	CCACCGGAG	CGGGGGTAC	GCCGTCACCA	CCGGCACCCG	1020
CGGTGGCCTT	GCCCGAGCCT	GCCGTCGCGG	TGGCACCGTC	GGCGCCGGTG	CCACCGGTG	1080
CGCTGCCGCG	AGTGCATGG	CCGCCGCTGC	CGCCGTCGCC	GCCGGTTGA	TCACCGATGC	1140
CGGACACATC	TGCCGGCTG	TCCCCGGTGC	TGGCCGCCGG	GCCGGGGCGTG	GGATTGACCC	1200
CGTTTGCCTT	GCGGAGGCCG	GGCGCGCCGG	TACCACCGGC	GCCGCCATGG	CCGAACAGCC	1260
CGGGCTTGCC	GCCGTTACCG	CCCGCACCCC	CGATGCCCTG	GGCACCGCTG	GTGCCGCCGA	1320
CACCCCGCTT	GCCGCCGTTG	CCCCAACAAAC	ACCCCCCGTT	CCCACCGGA	CCGGCGGCCG	1380
CGCCGGTACC	ACCGGCCCCG	CCGTTGCCGC	CGTTGCCGAT	CAACCCGGCC	GGCCTCCGC	1440
TGCCGCCGCTT	TTGACCGAAC	CCGCCAGCG	CGCCGTTGCC	ACCGTTGCCA	AACAGCAAC	1500
CGGGCCGCCG	GCCAGGCTGC	CGGGGTGCCG	TCCCCTGCCG	GGCGTTCCG	ATCAACGGGC	1560
GCCCCAAAAG	GCGCTCGGTG	GGCGCATTCA	CCGCACCCAG	CAGACTCCGC	TCAACAGCGG	1620
CTTCAGTGTCT	GGCATACCGA	CCCGCGGCCG	CAGTCACACG	CTGCACAAAC	TGCTCGTGAA	1680
ACGCTGCCAC	CTGTACGCTG	ACGCCTGTAT	ACTGCCGAGC	ATGGGCCCCG	AAACACCCCG	1740
CAATGCCGCG	CGACACTTCA	TGGCAGCCG	CAGCCACAC	TTCCGTCGTC	GGGATGCCG	1800
CGGGCGCATT	AGCCGCGCTC	ACCTGCGAAC	CAATAGTCGA	TAAATCCAAA	GCCGCAGTTG	1860

CCAGCAGCTG CGGCAGTCGCG ATCACCAAGG ACACCTCGCA CCTCCGGATA CCCCATATCG 1920  
 CGCGACCGTG TCCCCAGCGG CCACGTGACC TTTGGTCGCT GGCTGGCGGC CCTGACTATG 1980  
 GCGCGACGG CCCTCGTTCT GATTGCCCC GGCGCGCAGC TTGTTGCGCG AGTTGAAGAC 2040  
 GGGAGGACAG GCCGAGCTTG GTGTAGACGT GGGTCAAGTG GGAATGCACG GTCCGCGCG 2100  
 AGATGAATAG GCGGACCGC ATCTCCTTGT TGCTGAGTCC CTCACCGACC AGTAGAGCCA 2160  
 CCTCAAGCTC TGTCGGTGTG AACGCGCCCC AGCCACTTGT CGGGCGTTTC CGTGCACCGC 2220  
 GGCCCTCGTTG CGCGTACGCG ATCGCCTCAT CGATCGATAA CGCAGTTCT TCGGCCAGG 2280  
 CATCGTCGAA CTCGCTGTCA CCCATGGATT TTCGAAGGGT GGCTAGCGAC GAGTTACAGC 2340  
 CGGCCTGGTA GATCCCGAAG CGGACCG 2367

## (2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Gln Pro Ala Gly Ala Thr Ile Ala Ala Ser Ser Pro Cys Ala Thr Val  
 1 5 10 15

Gly Ala Gly Gly Gly Thr Gly Ser Pro Val Thr Thr Glu Thr Ala Ala  
 20 25 30

Thr Thr Gly Arg Gly Gly Ser Gly Asp Val Tyr Glu Ser Ala Ala Ser  
 35 40 45

Gly Ala Ala Ala Thr Thr Pro Thr Ala Gly Gly Tyr Thr Val Gly Pro  
 50 55 60

Val Ala Thr Ile Thr Ala Lys Gly Ala Arg Asn Val Ala Leu Arg Asp  
 65 70 75 80

Ser Ala Val Ala Ala Val Ala Ala Ala Thr Gly Ser Gly Gly Thr  
 85 90 95

Ala Val Thr Thr Gly Thr Ala Gly Gly Leu Ala Arg Ala Cys Arg Arg  
 100 105 110

Gly Gly Thr Val Ala Ala Gly Ala Thr Gly Arg Arg Ala Gly Ser Ala  
 115 120 125

Met Ala Ala Arg Ala Ala Val Ala Ala Gly Leu Ile Thr Asp Ala Gly  
 130 135 140

His Ile Cys Arg Ala Val Pro Gly Ala Gly Arg Gly Ala Gly Arg Gly  
 145 150 155 160  
 Ile Asp Pro Val Cys Pro Gly Glu Ala Gly Ala Ala Gly Thr Thr Gly  
 165 170 " 175  
 Ala Ala Met Ala Glu Gln Pro Gly Val Ala Ala Val Thr Ala Arg Thr  
 180 185 190  
 Pro Asp Ala Cys Gly His Ala Gly Ala Ala Asp Thr Ala Val Ala Ala  
 195 200 205  
 Val Ala Pro Gln Pro Pro Val Pro Thr Gly Thr Ala Gly Arg Ala  
 210 215 220  
 Gly Thr Thr Gly Pro Ala Val Ala Ala Val Ala Asp Gln Pro Gly Arg  
 225 230 235 240  
 Ala Ser Ala Ala Ala Gly Leu Thr Glu Pro Ala Ser Arg Ala Val Ala  
 245 250 255  
 Thr Val Ala Lys Gln Gln Pro Ala Gly Arg Ala Arg Leu Pro Gly Cys  
 260 265 270  
 Arg Pro Val Gly Ala Val Ser Asp Gln Arg Ala Pro Gln Lys Arg Leu  
 275 280 285  
 Gly Gly Arg Ile His Arg Thr Gln Gln Thr Pro Leu Asn Ser Gly Phe  
 290 295 300  
 Ser Ala Gly Ile Pro Thr Arg Gly Arg Ser Gln Arg Leu His Lys Leu  
 305 310 315 320  
 Leu Val Lys Arg Cys His Leu Tyr Ala Glu Arg Leu Ile Leu Pro Ser  
 325 330 335  
 Met Gly Pro Glu Gln Pro Arg Asn Arg Arg Arg His Phe Ile Gly Ser  
 340 345 350  
 Arg Ser His His Phe Arg Arg Arg Asp Arg Arg Gly Arg Ile Ser Arg  
 355 360 365  
 Ala His Leu Arg Thr Asn Ser Arg  
 370 375

## (2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2852 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

GGCCAAAACG	CCCCGGCGAT	CGCGGCCACC	GAGGCCGCCT	ACGACCAGAT	GTGGGCCAG	60
GACGTGGCGG	CGATGTTGG	CTACCATGCC	GGGGCTTCGG	CGGCCGTCTC	GGCGTTGACA	120
CCGTTCGGCC	AGGCGCTGCC	GACCGTGGCG	GGCGCGGTG	CGCTGGTCAG	CGCGGCCCGC	180
GCTCAGGTGA	CCACGCGGGT	CTTCCGCAAC	CTGGCTTGG	CGAACGTCCG	CGAGGGCAAC	240
GTCCGCAACG	GTAATGTCGG	GAACCTCAAT	CTCGGCTCGG	CCAACATCGG	CAACGGCAAC	300
ATCGGCAGCG	GCAACATCGG	CAGCTCAAC	ATCGGGTTTG	GCAACGTGGG	TCCTGGTTG	360
ACCGCAGCGC	TGAACACAT	CGGTTTCGGC	AACACCGGCA	GCAACAAACAT	CGGGTTGGC	420
AACACCCGCA	GCAACACAT	CGGGTTTCGGC	AATACCGGAG	ACGGCAACCG	AGGTATCGGG	480
CTCACGGTA	GGGGTTTGTG	GGGGTTTCGGC	GGCCTGAAC	CGGGCACCGG	CAACATCGGT	540
CTGTTCAACT	CGGGCACCGG	AAACGTCGGC	ATCGGCAACT	CGGGTACCGG	GAACTGGGC	600
ATTGGCAACT	CGGGCAACAG	CTACAAACACC	GGTTTTGGCA	ACTCCGGCGA	CGCCAACACG	660
GGCTTCTTCA	ACTCCGAAT	AGCCAACACC	GGCGTCGGCA	ACGCCGGCAA	CTACAAACACC	720
GGTAGCTACA	ACCCGGGCA	CAGCAATACC	GGCGGCTTCA	ACATGGGCCA	GTACAACACG	780
GGCTACCTGA	ACAGCGGCA	CTACAAACACC	GGCTTGGCA	ACTCCGGCAA	TGTCAACACC	840
GGCGCTTCA	TTACTGGCAA	CTTCAACAAAC	GGCTTCTTGT	GGCGCGGCGA	CCACCAAGGC	900
CTGATTTCG	GGAGCCCCGG	CTTCTTCAAC	TCGACCAGTG	CGCCGTCGTC	GGGATTCTTC	960
AACAGCGGTG	CGCGTAGCGC	GTCCGGCTTC	CTGAACCTCG	GTGCCAACAA	TTCTGGCTTC	1020
TTCAACTCTT	CGTCGGGGGC	CATCGTAAC	TCCGGCTTGG	CAAACGCGGG	CGTGTGGTA	1080
TCGGGCGTGA	TCAACTCGGG	CAACACCGTA	TCGGGTTTGT	TCAACATGAG	CCTGGTGGCC	1140
ATCACAACG	CGGGCTTGAT	CTCGGGCTTC	TTCAACACCG	GAAGCAACAT	GTGCGGATTT	1200
TTCGGGGCC	CACCGGTCTT	CAATCTCGC	CTGGCAAAC	GGGGCGTCTG	GAACATTCTC	1260
GGCAACGCCA	ACATCGGCAA	TTACAACATT	CTCGGAGCG	GAAACGTCGG	TGACTTCAAC	1320
ATCCTTGGCA	CGGGCAACCT	CGGCAGGCCA	AAACATCTTGG	GCAGCGGCAA	CGTCGGCAGC	1380
TTCAATATCG	GCAGTGGAAA	CATCGGAGTA	TTCAATGTCG	GTTCGGAAAG	CCTGGGAAAC	1440
TACAACATCG	GATCGGAAA	CCTCGGGATC	TACAACATCG	GTTCGGAAA	CGTCGGCAGC	1500
TACAACACGTG	GTTCGGAAA	CCTCGGGATC	TACAACATCG	GTTCGGAAA	CGTCGGCAGC	1560
AACAAACATCG	GGTCGCCAA	CACCGGCAAC	AACAAACATCG	GCATCGGGCT	GTCCGGCAGC	1620

AACCAAGCAGG GCTTCATAT TGCTAGCGGC TGGAACTCGG GCACCGGCAA CAGCGGCCCTG 1680  
 TTCAATTCTGG GCACCAATAA CGTTGGCATC TTCAACGCGG GCACCGGAAA CGTCGGCATC 1740  
 GCAAACCTCGG GCACCGGAA CTGGGGTATC GGGAACCCGG GTACCGACAA TACCGGCATC 1800  
 CTCAATGCTG GCAGCTACAA CACGGGCATC CTCAACGCGG GCGACTTCAA CACGGGCTTC 1860  
 TACAACACGG GCAGCTACAA CACCGGCGGC TTCAACGCTCG GTAACACCAA CACCGGCAAC 1920  
 TTCAACGTTG GTGACACCAA TACCGGCAGC TATAACCCGG GTGACACCAA CACCGGCTTC 1980  
 TTCAATCCCG GCAACGTCAA TACCGGCCTC TTGACACCGG GCGACTTCAA CAATGGCTTC 2040  
 TTGGTGGCGG GCGATAACCA GGGCCAGATT GCCATCGATC TCTCGGTACAC 2100  
 ATCCCCATAA ACGAGCAGAT GGTCAATTGAC GTACACAAACG TAATGACCTT CGCGGGCAAC 2160  
 ATGATCACCG TCACCGAGGC CTCGACCGTT TTCCCCAAA CCTTCTATCT GAGCGGTTTG 2220  
 TTCTTCTCTCG GCCCCGTCAA TCTCAGGCCA TCCACGCTGA CCGTTCGGAC GRTCACCCCTC 2280  
 ACCATCGGGC GACCGACGGT GACCGTCCCC ATCAGCATTG TCGGTGCTCT GGAGAGCCGC 2340  
 ACGATTACCT TCCTCAAGAT CGATCGGGC CCGGGCATCG GAAATTGAC CACCAACCCC 2400  
 TCGTCGGCT TCTTCACACTC GGGCACCGGT GGCACATCTG GCTTCCAAAA CGTCGGGGC 2460  
 GGCAGTTCACTAG CGCTCTGGAA CAGTGGTTTG AGCAGCGCGA TAGGGAATTG GGGTTTCCAG 2520  
 AACCTCGGCT CGCTCGAGTC AGGCTGGCG AACCTGGCA ACTCCGTATC GGGTTTTTC 2580  
 AACACCAAGTA CGGTGAACCT CTCCACGGC GCCAATGCT CGGGCGTCAA CAACATCGGC 2640  
 ACCAACCTGT CGCGCGTGTGTT CGCGCGTCCG ACCGGGACGA TTTCAACGC GGGCCTTGCC 2700  
 AACCTGGGCC AGTTGAACAT CGGCAGCGCC TCGTGGCGAA TTCGGCACGA GTTAGATACG 2760  
 GTTTCAACAA TCATATCCGC GTTTGGCGC AGTGCATCAG ACGAATCGAA CCCGGGAAGC 2820  
 GTAAAGCGAAT AAACCGAATG CGGGCGTGTCA AT 2852

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 943 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Gly Gln Asn Ala Pro Ala Ile Ala Ala Thr Glu Ala Ala Tyr Asp Gln

Met Trp Ala Gln Asp Val Ala Ala Met Phe Gly Tyr His Ala Gly Ala  
 20 25 30

Ser Ala Ala Val Ser Ala Leu Thr Pro Phe Gly Gln Ala Leu Pro Thr  
 35 40 45

Val Ala Gly Gly Gly Ala Leu Val Ser Ala Ala Ala Gln Val Thr  
 50 55 60

Thr Arg Val Phe Arg Asn Leu Gly Leu Ala Asn Val Arg Glu Gly Asn  
 65 70 75 80

Val Arg Asn Gly Asn Val Arg Asn Phe Asn Leu Gly Ser Ala Asn Ile  
 85 90 95

Gly Asn Gly Asn Ile Gly Ser Gly Asn Ile Gly Ser Ser Asn Ile Gly  
 100 105 110

Phe Gly Asn Val Gly Pro Gly Leu Thr Ala Ala Leu Asn Asn Ile Gly  
 115 120 125

Phe Gly Asn Thr Gly Ser Asn Asn Ile Gly Phe Gly Asn Thr Gly Ser  
 130 135 140

Asn Asn Ile Gly Phe Gly Asn Thr Gly Asp Gly Asn Arg Gly Ile Gly  
 145 150 155 160

Leu Thr Gly Ser Gly Leu Leu Gly Phe Gly Gly Leu Asn Ser Gly Thr  
 165 170 175

Gly Asn Ile Gly Leu Phe Asn Ser Gly Thr Gly Asn Val Gly Ile Gly  
 180 185 190

Asn Ser Gly Thr Gly Asn Trp Gly Ile Gly Asn Ser Gly Asn Ser Tyr  
 195 200 205

Asn Thr Gly Phe Gly Asn Ser Gly Asp Ala Asn Thr Gly Phe Phe Asn  
 210 215 220

Ser Gly Ile Ala Asn Thr Gly Val Gly Asn Ala Gly Asn Tyr Asn Thr  
 225 230 235 240

Gly Ser Tyr Asn Pro Gly Asn Ser Asn Thr Gly Gly Phe Asn Met Gly  
 245 250 255

Gln Tyr Asn Thr Gly Tyr Leu Asn Ser Gly Asn Tyr Asn Thr Gly Leu  
 260 265 270

Ala Asn Ser Gly Asn Val Asn Thr Gly Ala Phe Ile Thr Gly Asn Phe  
 275 280 285

Asn Asn Gly Phe Leu Trp Arg Gly Asp His Gln Gly Leu Ile Phe Gly  
 290 295 300

Ser Pro Gly Phe Phe Asn Ser Thr Ser Ala Pro Ser Ser Gly Phe Phe

305	310	315	320
Asn Ser Gly Ala Gly Ser Ala Ser Gly Phe Leu Asn Ser Gly Ala Asn			
325		330	335
Asn Ser Gly Phe Phe Asn Ser Ser Ser Gly Ala Ile-Gly Asn Ser Gly			
340	345		350
Leu Ala Asn Ala Gly Val Leu Val Ser Gly Val Ile Asn Ser Gly Asn			
355	360	365	
Thr Val Ser Gly Leu Phe Asn Met Ser Leu Val Ala Ile Thr Thr Pro			
370	375	380	
Ala Leu Ile Ser Gly Phe Phe Asn Thr Gly Ser Asn Met Ser Gly Phe			
385	390	395	400
Phe Gly Gly Pro Pro Val Phe Asn Leu Gly Leu Ala Asn Arg Gly Val			
405	410	415	
Val Asn Ile Leu Gly Asn Ala Asn Ile Gly Asn Tyr Asn Ile Leu Gly			
420	425	430	
Ser Gly Asn Val Gly Asp Phe Asn Ile Leu Gly Ser Gly Asn Leu Gly			
435	440	445	
Ser Gln Asn Ile Leu Gly Ser Gly Asn Val Gly Ser Phe Asn Ile Gly			
450	455	460	
Ser Gly Asn Ile Gly Val Phe Asn Val Gly Ser Gly Ser Leu Gly Asn			
465	470	475	480
Tyr Asn Ile Gly Ser Gly Asn Leu Gly Ile Tyr Asn Ile Gly Phe Gly			
485	490	495	
Asn Val Gly Asp Tyr Asn Val Gly Phe Gly Asn Ala Gly Asp Phe Asn			
500	505	510	
Gln Gly Phe Ala Asn Thr Gly Asn Asn Asn Ile Gly Phe Ala Asn Thr			
515	520	525	
Gly Asn Asn Asn Ile Gly Ile Gly Leu Ser Gly Asp Asn Gln Gln Gly			
530	535	540	
Phe Asn Ile Ala Ser Gly Trp Asn Ser Gly Thr Gly Asn Ser Gly Leu			
545	550	555	560
Phe Asn Ser Gly Thr Asn Asn Val Gly Ile Phe Asn Ala Gly Thr Gly			
565	570	575	
Asn Val Gly Ile Ala Asn Ser Gly Thr Gly Asn Trp Gly Ile Gly Asn			
580	585	590	
Pro Gly Thr Asp Asn Thr Gly Ile Leu Asn Ala Gly Ser Tyr Asn Thr			
595	600	605	

Gly Ile Leu Asn Ala Gly Asp Phe Asn Thr Gly Phe Tyr Asn Thr Gly  
 610 615 620  
 Ser Tyr Asn Thr Gly Gly Phe Asn Val Gly Asn Thr Asn Thr Gly Asn  
 625 630 635 640  
 Phe Asn Val Gly Asp Thr Asn Thr Gly Ser Tyr Asn Pro Gly Asp Thr  
 645 650 655  
 Asn Thr Gly Phe Phe Asn Pro Gly Asn Val Asn Thr Gly Ala Phe Asp  
 660 665 670  
 Thr Gly Asp Phe Asn Asn Gly Phe Leu Val Ala Gly Asp Asn Gln Gly  
 675 680 685  
 Gln Ile Ala Ile Asp Leu Ser Val Thr Thr Pro Phe Ile Pro Ile Asn  
 690 695 700  
 Glu Gln Met Val Ile Asp Val His Asn Val Met Thr Phe Gly Gly Asn  
 705 710 715 720  
 Met Ile Thr Val Thr Glu Ala Ser Thr Val Phe Pro Gln Thr Phe Tyr  
 725 730 735  
 Leu Ser Gly Leu Phe Phe Phe Gly Pro Val Asn Leu Ser Ala Ser Thr  
 740 745 750  
 Leu Thr Val Pro Thr Ile Thr Leu Thr Ile Gly Gly Pro Thr Val Thr  
 755 760 765  
 Val Pro Ile Ser Ile Val Gly Ala Leu Glu Ser Arg Thr Ile Thr Phe  
 770 775 780  
 Leu Lys Ile Asp Pro Ala Pro Gly Ile Gly Asn Ser Thr Thr Asn Pro  
 785 790 795 800  
 Ser Ser Gly Phe Phe Asn Ser Gly Thr Gly Gly Thr Ser Gly Phe Gln  
 805 810 815  
 Asn Val Gly Gly Ser Ser Gly Val Trp Asn Ser Gly Leu Ser Ser  
 820 825 830  
 Ala Ile Gly Asn Ser Gly Phe Gln Asn Leu Gly Ser Leu Gln Ser Gly  
 835 840 845  
 Trp Ala Asn Leu Gly Asn Ser Val Ser Gly Phe Phe Asn Thr Ser Thr  
 850 855 860  
 Val Asn Leu Ser Thr Pro Ala Asn Val Ser Gly Leu Asn Asn Ile Gly  
 865 870 875 880  
 Thr Asn Leu Ser Gly Val Phe Arg Gly Pro Thr Gly Thr Ile Phe Asn  
 885 890 895

Ala Gly Leu Ala Asn Leu Gly Gln Leu Asn Ile Gly Ser Ala Ser Cys  
 900 905 910

Arg Ile Arg His Glu Leu Asp Thr Val Ser Thr Ile Ile Ser Ala Phe  
 915 920 925

Cys Gly Ser Ala Ser Asp Glu Ser Asn Pro Gly Ser Val Ser Glu  
 930 935 940

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

GGATCCATAT GGGCCATCAT CATCATCATC ACGTGATCGA CATCATCGGG ACC 53

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

CCTGAATTCA GGCCTCGGTT GCGCCGGCCT CATCTTGAAC GA 42

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

GGATCCTGCA GGCTCGAAC CACCGAGCGG T 31

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

CTCTGAATTC AGCGCTGGAA ATCGTCGCGA T

31

## (2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GGATCCAGCG CTGAGATGAA GACCGATGCC GCT

33

## (2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GGATATCTGC AGAATTCAAGG TTTAAAGCCC ATTTGCGA

38

## (2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

CCGCATGCGA GCCACGTGCC CACAACGGCC

30

## (2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

CTTCATGGAA TTCTCAGGCC GGTAAGGTCC GCTGCGG

37

## (2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7676 base pairs
- (B) TYPE: nucleic acid

10084843 - 022502

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

TGGCGAATGG GACGCGCCCT GTAGCGGCGC ATTAAGCGCG GCGGGGTGTTG TGGTTACGCG	60
CAGCGTGACC GCTACACTTG CCAGCGCCCT AGCGCCCGCT CCTTTCGCTT TCTTCCCTTC	120
CTTTCTCGCC ACGTTCGCG GCTTCCCCG TCAAGCTCTA AATCGGGGGC TCCCTTTAGG	180
GTTCCGATT AGTGCTTAC GGCACCTCGA CCCAAAAAA CTTGATTAGG GTGATGGTTC	240
ACGTAGTGGG CCATCGCCCT GATAGACGGT TTTTCGCCCT TTGACGTTGG AGTCCACGTT	300
CTTTAATAGT GGACTCTGT TCCAAACTGG AACAAACACTC AACCTATCT CGGTCTATTCT	360
TTTTGATTAA TAAGGGATT TGCGGATTTG GGCCTATTGG TTAAAAAATG AGCTGATTAA	420
ACAAAAAATT AACGCGAATT TTAACAAAAT ATTAACGTTT ACAATTTCAG GTGGCACTTT	480
TGGGGGAAAT GTGCGCGAA CCCCTATTG TTTATTTTC TAAATACATT CAAATATGTA	540
TCCGCTCATG AATTAATTCT TAGAAAAACT CATCGAGCAT CAAATGAAAC TGCAATTAT	600
TCATATCAGG ATTATCAATA CCATATTGTT GAAAAAGCCG TTTCTGTAAT GAAGGAGAAA	660
ACTCACCAG GCAGTTCCAT AGGATGGCA GATCCTGGTA TCGGTCTCGG ATTCCGACTC	720
GTCCAACATC AATACAACCT ATTAATTCC CCTCGTCAAA AATAAGGTTA TCAAGTGAGA	780
AATCACCATG AGTGACGACT GAATCCGGTG AGAATGGCAA AAGTTTATGC ATTTCTTCC	840
AGACTTGTTC AACAGGCCAG CCATTACGCT CGTCATCAAA ATCACTCGCA TCAACCAAAC	900
CGTTATTCTAT TCCTGATTGC GCCTGAGCGA GACGAAATAC GCGATCGCTG TTAAAGGAC	960
AATTACAAAC AGGAATCGAA TGCAACCGGC GCAGGAAACAC TGCCAGCGCA TCAACAAATAT	1020
TTTCACCTGA ATCAGGATAT TCTTCTAATA CCTGGATGC TGTGTTCCCG GGGATCGCAG	1080
TGGTAGTAA CCATGCATCA TCAGGAGTAC GGATAAAATG CTTGATGGTC GGAAGAGGCA	1140
TAAATTCCGT CAGCCAGTT AGTCTGACCA TCTCATCTGT AACATCATTG GCAACGCTAC	1200
CTTTGCATG TTTCAGAAC AACCTCGCG CATCGGGCTT CCCATACAAAT CGATAGATG	1260
TGCGACCTGA TTGCCCCGACA TTATCGCGAG CCCATTTATA CCCATATAAA TCAGCATCCA	1320
TGTTGGAATT TAATCGCGGC CTAGAGCAAG ACGTTCCCG TTGAATATGG CTCATAACAC	1380
CCCTTGATT ACTGTTATG TAAGCAGACA GTTTTATGTC TCACTGACCAA AATCCCTTAA	1440
CGTGAGTTT CGTCCACTG AGCGTCAGAC CCCGTAGAAA AGATCAAAGG ATCTTCTTGA	1500

GATCCTTTT TTCTGCGCGT AATCTGCTGC TTGCAAACAA AAAAACACC GCTACCAGCG	1560
GTGGTTGTT TGCGGATCA AGAGCTACCA ACTCTTTTC CGAAGGTAAC TGGCTTCAGC	1620
AGAGCGCAGA TACCAAATAC TGTCCTCTA GTGTAGCCGT AGTTAGGCCA CCACATTCAAG	1680
AACTCTGTAG CACCGCCTAC ATACCTCGCT CTGCTAATCC TGTTACCAGT GGCTGCTGCC	1740
AGTGGCGATA AGTCGTGTCT TACCGGGTGTG GACTCAAGAC GATAGTTACCG GGATAAGGGC	1800
CAGCGGTCGG GCTGAACGGG GGGTCGTGC ACACAGCCCA GCTTGGAGCG AACGACCTAC	1860
ACCGAACTGA GATACTACA GCGTGAGCTA TGAGAAAGCG CCACGCTTCC CGAAGGGAGA	1920
AAGGCGGACA GGTATCCGGT AAGCGGCAGG GTCCGGAACAG GAGAGCGCAG GAGGGAGCTT	1980
CCAGGGGAA ACGCCTGGTA TCTTTATAGT CCTGTGGGT TTCGCCACCT CTGACTTGAG	2040
CGTCGATTTT TGTGATGCTC GTCAAGGGGG CGGAGCCCTAT GGAAAACCGC CAGCACGCG	2100
GCCTTTTAC GGTCCTGGC CTTTGCTGG CCTTTGCTC ACATGTTCTT TCCTGCTTA	2160
TCCCCGTGATT CTGTGATAA CCGTATTACCG CCGTTTGAGT GAGCTGATAC CGCTCGCCCG	2220
AGCGAACGA CCGAGCGCAG CGAGTCAGTG AGCGAGGAAG CGGAAGAGCG CCTGATGCGG	2280
TATTTTCTCC TTACGCATCT GTGCGGTATT TCACACCGCA TATATGGTGC ACTCTCAGTA	2340
CAATCTGCTC TGATGCCGCA TAGTTAACCG AGTATACACT CCGCTATCGC TACGTGACTG	2400
GGTCATGGCT GCGCCCGAC ACCCGCAAC ACCCGCTGAC GCGCCCTGAC GGGCTTGCT	2460
GCTCCCGGCA TCCGCTTACA GACAAGCTGT GACCGCTCC GGGAGCTGCA TGTGTCAGAG	2520
GTTTCAACCG TCATCACCGA AACGCGCAG GCGACTGCGG TAAAGCTCAT CAGCGTGGTC	2580
GTGAAGCGAT TCACAGATGT CTGCGCTTTC ATCCGCTGCC AGCTCGTTGA GTTCTCCAG	2640
AAGCGTTAAT GTCTGGCTTC TGATAAACCGG GGCCATGTAA AGGGCGTTT TTCTGTTT	2700
GGTCACTGAT GCCTCCGTGT AAGGGGGATT TCTGTTCATG GGGTAATGAA TACCGATGAA	2760
ACGAGAGAGG ATGCTCACGA TACGGGTTAC TGATGATGAA CATGCCCGGT TACTGGAACG	2820
TTGTGAGGGT AAACAACCTGG CGGTATGGAT GCGGCGGGAC CAGAGAAAAA TCACTCAGGG	2880
TCAATGCCAG CGCTTCGTAA ATACAGATGT AGGTGTTCA CAGGGTAGCC AGCAGCATCC	2940
TGCGATGCCAG ATCCGGAACA TAATGGTGCAG GGGCGCTGAC TTCCGCGTTT CCAGACTTTA	3000
CGAAACACCGG AAACCGAAGA CCATTCTATGT TGTTGCTCAG GTCCGAGACG TTTTGCAGCA	3060
GCAGTCGCTT CACGTTCGCT CGCGTATCGG TGATTCAATTC TGCTAACCCAG TAAGGCAACC	3120
CCGCCAGCCT AGCCGGGTCC TCAACGACAG GAGCACGATC ATGCGCACCC GTGGGGCCGC	3180

CATGCCGGCG ATAATGGCT GCTTCTGCC GAAACGTTG GTGCCGGGC CAGTGA  
GGCTTGAGCG AGGGCGTGCA AGATTCGAA TACCGCAAGC GACAGGCCA TCATCGTC  
GCTCCAGCGA AAGCGGTCT CGCCGAAAAT GACCCAGAGC GCTGCCGGCA CCTGTC  
GAGTTGCATG ATAAAAGAAGA CAGTCATAAG TGCGGCAGC ATAGTCATG CCCGCG  
CCGGAAGGAG CTGACTGGGT TGAAGGCTCT CAAGGGCATH GGTCGAGATC CCGGTG  
ATGAGTGAGC TAACCTTACAT TAATTGCGTT GCGCTCACTG CCCGCTTCC AGTCGG  
CCTGTCGTGC CAGCTGCATT ATGAATCGG CCAACGCGCG GGGAGAGGC GTTTGC  
TGGCGCCAG GGTGGTTTTT CTTTCACCA GTGAGACGGG CAACAGCTGA TTGCC  
CCGCCTGGCC CTGAGAGAGT TGCAAGCAAGC GGTCCACGCT GGTTTGCCCC AGCAGGC  
AATCCTGTT GATGGTGGTT AACGGCGGA TATAACATGA GCTGTC  
ATCCCAC  
TACAGATATCC GCACCAACGC GCAGCCGGGA CTGGTAAATG GCGCGCATTG  
CGCC  
CAGCGC CATCTGATCG TTGCAACCA GCATCGCAGT GGGAACGATG CCCTCATTCA  
GCATTG  
CATGGTTGTA AAACCGGACA TGCGACTCCA GTGCC  
CTTCCGCTA  
TCGGCTGAAT TTGATTGCGA GTGAGATATT TATGCCAGCC AGCCAGACGC AGACGCG  
AGACAGAACT TAATGGGCC GCTAACAGCG CGATTGCTG GTGACCC  
GCGACCAGAT  
GCTCCACGCC CAGTCGCGTA CGCTTCTCAT GGGAGAAAAT AATACTGTT ATGGGTG  
GGTCAGAGAC ATCAAGAAA AACGCCGGAA CATTAGTGC  
GGCAGCTTCC ACAGCAATGG  
CATCCTGGTC ATCCAGCGGA TAGTTAATGA TCAGCC  
ACT GACCGTTC GCGAGAAGAT  
TGTGCACCGC CGCTTTACAG GCTTCTGCGC CGCTTCTGTC TACCATCGC ACCACCC  
TGGCACCCAG TTGATCGCGC CGAGATTAA TCGCCGCGAC AATTGCGAC  
GGCAGCTGCA  
GGGCCAGACT GGAGGTGGCA ACGCCAATCA GCAACGACTG TTG  
GCCGCCAGC AGTTGTTG  
CCACGCGGTT GGGAAATGTA TTCAGCTCG CCATCGCGC  
TTTCACTTTT TCCCGCGTT  
TCGCAGAAAC TTGCGCTGGC TGGTTCACCA CGCGGGAAAC GGTCTGATAA GAGACACCGG  
CATACTCTGC GACATCGTAT AACGCTTACTG GTTTCACATT CAC  
CACCACCC  
AATTGACTCT  
CTTCCGGCGC CTATCATGCC ATACCGCGAA AGG  
GTTTGC  
GCG CCATTGAGT G  
TGTGCCGGGA  
TCTCGACGCT CTCCCTTATG CGACTCTGC ATTAGGAAGC AGCCAGTAG TAGGTTGAGG  
CCGTTGAGCA CGCGCGCCGC AAGGAATGGT GCATGCAAGG AGATGGGCC  
CAACAGTCCC

CGGGCCACGG GGCCTGCCAC CATAACCACG CGAAACAAAG CGCTCATGAG CCCGAAGTGG 4860  
 CGAGCCGAT CTTCCCCATC GGTGATGTCG GCGATATAAG CGCCAGCAG CGCACCTGTG 4920  
 GGCCTGGTGA TGCCGGCCAC GATGCGTCCG GCGTAGAGGA TCGAGATCTC GATCCCGCGA 4980  
 AATTAATACG ACTCACTATA GGGAAATTGT GAGCGGATAA CAATTCCCT CTAGAAATAA 5040  
 TTTGTTAA CTTAAAGAAG GAGATATACA TATGGCCAT CATCATCATC ATCACGTGAT 5100  
 CGACATCATC GGGACCAGCC CCACATCTG GGAACAGCG CGCCGGGAGG CGTCCAGCG 5160  
 GGCCTGGGAT AGCGTCGATG ACATCCCGT CGCTCGGTC ATTGAGCAGG ACATGGCCGT 5220  
 GGACAGCGCC GGCAAGATCA CCTACCCAT CAAGCTCGAA GTGCGTCA AGATGAGGCC 5280  
 GGCGCAACCG AGGGGCTCGA AACCAACCGAG CGGTTCGCCT GAAACGGCG CGGGCGCCCG 5340  
 TACTGTCGCG ACTACCCCG CGTCGTCGCC GGTGACGTTG GCGGAGACCG GTAGCAGCCT 5400  
 GCTCTACCCG CTGTTCAACCG TGTGGGTCG GGCCTTCAC GAGAGGTATC CGAACGTCAC 5460  
 GATCACCGCT CAGGGCACCG GTTCTGGTGC CGGGATCGCG CAGGCCGCCG CGGGACGGT 5520  
 CAACATTGGG GCCTCCGACG CCTATCTGTC GGAAGGTGAT ATGGCCGCGC ACAAGGGCT 5580  
 GATGAACATC GCGCTAGCCA TCTCCGCTCA GCAGGTCAC TACAACTGC CGGGAGTGA 5640  
 CGAGCACCTC AAGCTGAACG GAAAAGTCCT GGCGGCCATG TACCAGGGCA CCATCAAAC 5700  
 CTGGGACGAC CGCGAGATCG CTGCGCTCAA CCCCCTGGTGA AACCTGCCG GCACCGCGGT 5760  
 AGTTCCTGCTG CACCGCTCCG ACGGGTCGCG TGACACCTTC TTGTTCACCC AGTACCTGTC 5820  
 CAAGCAAGAT CCCGAGGGCT GGGGCAAGTC GCCCGCTTC GGCACCCACCG TCGACTTCCC 5880  
 GGCCTGGCCG GGTGCGCTGG GTGAGAACCG CAACGGCGGC ATGGTGACCG GTTGCGCCGA 5940  
 GACACCGGGC TGCCTGGCT ATATCGGCAT CAGCTTCCCT GACCAGGGCA GTCAACGGGG 6000  
 ACTCGCGAG GCCCAACTAG GCAATAGCTC TGGCAATTTC TTGTTGCCG ACACCGCAAAG 6060  
 CATTCAAGGCC GCGGCGGGCTG GCTTCGCTAC GAAAACCCCG GCGAACCCAGG CGATTTCGAT 6120  
 GATCGACGGG CCCGCCCGG ACGGCTACCC GATCATCAAC TACGAGTACG CCATCGTCAA 6180  
 CAACCGGCAA AAGGACGCCG CCACCGCGCA GACCTTGAG GCATTTCTGC ACTGGGCGAT 6240  
 CACCGACGGC AACAAAGGCCT CGTTCTCGA CCAGGTTCAT TTCCAGGCCG TGCCGCCCGC 6300  
 GGTGGTGAAG TTGTCGACG CGTTGATCGC GACGATTCC AGCGCTGAGA TGAAGACCGA 6360  
 TGCCGCTTAC CTCGCGCAGG AGGCAGGTTA TTTCGAGCGG ATCTCCGGCG ACCTGAAAAC 6420  
 CCAGATCGAC CAGGTGGAGT CGACGGCAGG TTCTGAGCAG GGCCAGTGGC GCACCGCGGC 6480

GGGGACGGCC GCCCAGGCC CGGTGGTGC GCTCCAAGAA GCAGCCAATA AGCAGAAC 6540  
 GGAACTCGAC GAGATCTCGA CGAATATTG TCAGGCCGGC GTCCAATACT CGAGGGCCGA 6600  
 CGAGGAGCGAG CAGCAGGCC TGTCCTCGCA AATGGGCTTT GTGCCACAA CGGCCGCCTC 6660  
 GCCGCCGCTCG ACCGCTGCAG CGCCACCCGC ACCGGGACAA CCTGTTGCC CCCCCACCAC 6720  
 GGCCGCCGCC AACACGCCGA ATGCCAGCC GGGCGATCCC AACGCAGCAG CTCCGCCGGC 6780  
 CGACCCGAAC GCACCGCCGC CACCTGTCA TGCCCCAAC GCACCCAAC CTGTCCGGAT 6840  
 CGACAAACCG GTTGGAGGGAT TCAGCTTCGC GCTGCCCTGCT GGCTGGGTGG AGTCTGACGC 6900  
 CGCCCACTTC GACTACGGTT CAGCCTCTC CAGCAAAACC ACCGGGGACCG CGCCATTTC 6960  
 CGGACAGCCG CGGCCGGTGG CCAATGACAC CCGTATCGTG CTGGCCGGC TAGACCAAA 7020  
 GCTTTACGCC AGCGCCGAAG CCACCGACTC CAAGGGCGCG GCGCGGTGG GCTCGGACAT 7080  
 GGGTGAGGTC TATATGCCCT ACCCGGGCAC CGGATCAAC CAGGAAACCG TCTCGCTTGA 7140  
 CGCCAAACGGG GTCTCTGGAA GCGCGCTGTA TTACGAAGTC AAGTTCAGCG ATCCGAGTAA 7200  
 CGCGAACGGC CAGATCTGGA CGGGCGTAAT CGGCTCGCC CGGGCGAACG CACCGGACGC 7260  
 CGGGCCCTCT CAGCGCTGGT TTGTGGTATG GCTCGGGACC GCAACAAACC CGGTGGACAA 7320  
 GGGCGCCGCC AAGGCCTGCG CCGAATCGAT CGGGCCTTTG GTCGCCCCCG CGCCCGGCC 7380  
 GGCACCGGCT CCTGCAGAGC CGCCTCCGGC GCGGGCGCCG GCGGGGGAAAG TCGCTCCTAC 7440  
 CCCGACGACA CGCACACCGC AGCGGACCTT ACCGGCCTGA GAATCTGCA GATATCCATC 7500  
 ACACCTGGCGG CGCCTCGAGC ACCACCAACCA CCACCACTGA GATCGGGCTG CTAACAAAGC 7560  
 CCGAAAGGAA GCTGAGTTGG CTGCTGCCAC CGCTGAGCAA TAACTAGCAT AACCCCTTGG 7620  
 GGCCTCTAAA CGGGTCTTGA GGGGTTTTT GCTGAAAGGA GGAACCTATAC CCGGAT 7676

## (2) INFORMATION FOR SEQ ID NO:214:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Met	Gly	His	His	His	His	His	His	Val	Ile	Asp	Ile	Ile	Gly	Thr	Ser
1															

Pro	Thr	Ser	Trp	Glu	Gln	Ala	Ala	Ala	Glu	Ala	Val	Gln	Arg	Ala	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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20

25

30

Asp Ser Val Asp Asp Ile Arg Val Ala Arg Val Ile Glu Gln Asp Met  
 35 40 45  
 Ala Val Asp Ser Ala Gly Lys Ile Thr Tyr Arg Ile Lys Leu Glu Val  
 50 55 60  
 Ser Phe Lys Met Arg Pro Ala Gln Pro Arg Gly Ser Lys Pro Pro Ser  
 65 70 75 80  
 Gly Ser Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro  
 85 90 95  
 Ala Ser Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr  
 100 105 110  
 Pro Leu Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn  
 115 120 125  
 Val Thr Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln  
 130 135 140  
 Ala Ala Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser  
 145 150 155 160  
 Glu Gly Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala  
 165 170 175  
 Ile Ser Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His  
 180 185 190  
 Leu Lys Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile  
 195 200 205  
 Lys Thr Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn  
 210 215 220  
 Leu Pro Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly  
 225 230 235 240  
 Asp Thr Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly  
 245 250 255  
 Trp Gly Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val  
 260 265 270  
 Pro Gly Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys  
 275 280 285  
 Ala Glu Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp  
 290 295 300  
 Gln Ala Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser  
 305 310 315 320

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Gly Asn Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala  
 325 330 335  
 Gly Phe Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp  
 340 345 350  
 Gly Pro Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile  
 355 360 365  
 Val Asn Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala  
 370 375 380  
 Phe Leu His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp  
 385 390 395 400  
 Gln Val His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp  
 405 410 415  
 Ala Leu Ile Ala Thr Ile Ser Ser Ala Glu Met Lys Thr Asp Ala Ala  
 420 425 430  
 Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile Ser Gly Asp Leu  
 435 440 445  
 Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln Gly  
 450 455 460  
 Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala Ala Val Val Arg  
 465 470 475 480  
 Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile Ser  
 485 490 495  
 Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu Glu  
 500 505 510  
 Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe Val Pro Thr Thr Ala  
 515 520 525  
 Ala Ser Pro Pro Ser Thr Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro  
 530 535 540  
 Val Ala Pro Pro Pro Pro Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro  
 545 550 555 560  
 Gly Asp Pro Asn Ala Ala Pro Pro Ala Asp Pro Asn Ala Pro Pro  
 565 570 575  
 Pro Pro Val Ile Ala Pro Asn Ala Pro Gln Pro Val Arg Ile Asp Asn  
 580 585 590  
 Pro Val Gly Gly Phe Ser Phe Ala Leu Pro Ala Gly Trp Val Glu Ser  
 595 600 605

205220-24843000

Asp Ala Ala His Phe Asp Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr  
 610 615 620  
 Gly Asp Pro Pro Phe Pro Gly Gln Pro Pro Pro Val Ala Asn Asp Thr  
 625 630 635 640  
 Arg Ile Val Leu Gly Arg Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu  
 645 650 655  
 Ala Thr Asp Ser Lys Ala Ala Ala Arg Leu Gly Ser Asp Met Gly Glu  
 660 665 670  
 Phe Tyr Met Pro Tyr Pro Gly Thr Arg Ile Asn Gln Glu Thr Val Ser  
 675 680 685  
 Leu Asp Ala Asn Gly Val Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys  
 690 695 700  
 Phe Ser Asp Pro Ser Lys Pro Asn Gly Gln Ile Trp Thr Gly Val Ile  
 705 710 715 720  
 Gly Ser Pro Ala Ala Asn Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp  
 725 730 735  
 Phe Val Val Trp Leu Gly Thr Ala Asn Asn Pro Val Asp Lys Gly Ala  
 740 745 750  
 Ala Lys Ala Leu Ala Glu Ser Ile Arg Pro Leu Val Ala Pro Pro Pro  
 755 760 765  
 Ala Pro Ala Pro Ala Pro Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala  
 770 775 780  
 Gly Glu Val Ala Pro Thr Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu  
 785 790 795 800  
 Pro Ala

## (2) INFORMATION FOR SEQ ID NO:215:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

GTGGCGGCCG	TGCGGGCCGG	CAGCAGAGCG	ATGTGCATCC	GTTCGCGAAC	CTGATCGCGG	60
TCGACGATGA	GGCGCGCCGAA	CGCCCGGACG	ACGAAGAACG	TCAGGAAGCC	GTCCAGCAGC	120
GCGGTCGGCG	CGGTGACGAA	GCTGACCCCG	TCGAGATCA	GCAGCACCCC	GGCGATGGCG	180
CCGACACATG	TCGACCCGGCT	GATCCGGCG	ACGATCCGCA	CCACCAAGCGC	CACCAAGGACC	240
ACACCCAGCA	GGCGCGCCGCT	GAACCGGCG	CCGAATCCGT	TGTGACCGAA	GATGGCCTCC	300

CCGATCGCGA	TCAGCTGCTT	ACCGACCGGC	GGGTGAACCA	CCAGGCCGTA	CCGGGGTTG	360
TCTTCACCC	CATGGTGTGTT	CAGCACCTGC	CAGGCCCTGGC	GGTGCCTAAT	GCTTCTCGTC	420
GAAGATGGGG	GTGCCGGCAT	CCGTCACCGA	GCCCG			454

## (2) INFORMATION FOR SEQ ID NO:216:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

TGCAAGAGTA	CGGGGGATCC	TCGGTGGCCG	ACGCCGAACG	GATTGCCCG	GTCGCCAAC	60
GCATCGTCG	CACCAAGAAG	CAAGGCAATG	ACGTCGTCGT	CGTCGTCCT	GCCATGGGGG	120
ATACCCCGA	CGACCTGCTG	GATCTGCTTC	AGCAGGTGTG	CCCGGGGCGC	CGGCCCTCGGG	180
AGCTGGACAT	GCTGTTAAC	GGCGGTGAAC	GCATCTGAA	TGGGTGGGTG	GCCATGGCCA	240
TCGAGTCGCT	CGGGCGCAT	GCCGGTGTGT	TCACCGGTTG	GCAGGCCGGG	GTGATCACCA	300
CCGGCACCCA	CGGAACGCC	AAAGATCATCG	AGCTCACGCC	GGGGCGGTG	CAAACCGCCC	360
TTGAGGAAGG	CGGGTGCCTG	TTGGTGGCCG	GATTCAAGG	GGTCAGCCAG	GACACCAAGG	420
ATGTCACGAC	GTTGGGCCGC	GGCGGCTCGG	ACACCAACGC	CGTCGCCATG		470

## (2) INFORMATION FOR SEQ ID NO:217:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

GGCCGGCGTA	CCCGGGCGGG	ACAAACAAACG	ATCGATTGAT	ATCGATGAGA	GACGGAGGAA	60
TCTGTTCCCT	TCCCCAGTTG	ACCGACGAGC	AGCGCGCGC	CGCGTTGGAG	AAGGCTGCTG	120
CCGCACTCG	GGCGGACCA	GAGCTCAAGG	ATCGCTCAA	CGCTGGGGC	ACCAACCTCA	180
CCCAGGTTCT	CAAGGACCCG	GAGAGCGATG	AAGTCTGGG	CAAATGAAG	GTGTCCTGCG	240
TCGTTGAGGC	CTTGCCAAAG	GTGGGCAAGG	TCCAGCGC			279

## (2) INFORMATION FOR SEQ ID NO:218:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

ACACGGTCGA	ACTCGACGAG	CCCTCGTGG	AGGTGTCGAC	CGACAAGGTC	GACACCGAAA	60
TCCCTCGCCG	GCCGCGGGTG	TGCTGACCAA	GATCATCGCC	CAAGAAGATG	ACACGGTCGA	120
GGTCGGGGC	GAGCTCTCTG	TCATIGGGCA	CGCCCCATGAT	GCCGGCAGGG	CGCGGGTCCC	180
GGCACCCCG	AAAGTCTCTG	CCGGCCCAAC	CCGAATCCA			219

## (2) INFORMATION FOR SEQ ID NO:219:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TCGCTGCCGA	CATCGGCCG	GGCGCCGCC	CCAAGCCGC	ACCCAAGCCC	GTCCCCGAGC	60
CAGCGGCCAC	GCGGAAGGCC	GAACCCGAC	CATCGCCCG	GGCGGCCAG	CCAGCCCGTG	120
CGGGCGAGGG	CGCACCGTAC	GTGACGCCGC	TGGTGCAGAAA	GCTGGCGTGC	AAAAACAAACAA	180
TCGACCTCCG	CGGGGTGACC	GGCACCGGAG	TGGGGTGTG	CATCCGAAAA	CAGGATGTGC	240
TGGCCGGGCG	TGAACAAAG	AAGCGGGCGA	AAGGCACCGGC	GCCGGCCGCC	CAGGCCGCCG	300
CCGCGCCGGC	CCCGAACAGCG	CGCGCTGAAAG	ATCCGATGCC	GC		342

## (2) INFORMATION FOR SEQ ID NO:220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

GGGTCTTGGT	CAGTATCAGC	GCGGACGAGG	ACGCCACGGT	GCCCGTGGC	GGCGAGTTGG	60
CCCGGATCGG	TGTCGCTGCC	GACATCGGCC	CGCGGCCCGC	CCCCAAGCCC	GCACCCAAAGC	120
CCGTCGGCGG	GCCAGCGGGC	ACGCCGAAGG	CCGAACCCGC	ACCATCGCCG	CCGGCGGCCCG	180
AGCCAGCGG	TGGGGCGAGG	GGCGCACCGT	ACGTGACGCC	GCTGGTGGA	AAAGCTGGCGT	240
CGGAAACCAA	CATCGACCTCA	GCCGGGGTGA	CGCCGACCCGG	AGTGGGTGGT	CGCATCCGCCA	300
AAACAGGATGT	GCTGGCGCGG	GCTGAACAAA	AGAACGGGG	GAAAGCACCG	GGCCCCCTGAG	360
CGCTTCATCA	CCCGGTAAAC	CAGCTTGGCC	CAGAAACCGG	CTTCGACCTC	TTCGCGGGTC	420
TTGGTCCGCT	GCAGGGCGGT	GGCGAGCAG	TTCAGGTAG	GGGCCGAAA	TCTTCCAGTT	480
CGCCAGGAAG	GGCACCCGGA	ACAGGGTCCG	CACCC			515

## (2) INFORMATION FOR SEQ ID NO:221:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

CCGACCCCCA	GGTGCAGATT	CAACAGGCCA	TTGAGGAAGC	ACAGCGCACC	CACCAAGCGC	60
TGACTCAACA	GGCGCGCGAA	GTGATCGGTA	ACCAAGCGTCA	ATTGGAGATG	CGACTCAACC	120
GACAGCTGG	GGACATCGAA	AAGCTTCAGG	TCAATGTGCG	CCAAGCCCTG	ACGCTGCGCG	180
ACCAGGCCAC	GGCGCCCGGA	GACGCTCGCA	AGGCCACCGA	ATACAAACAC	GCGGCCGAGG	240
CGTTCGCGC	CGAGCTGGTG	ACCGCCGAGC	AGAGCGTCCGA	AGAACCTCAAG	ACGCTGCGATG	300
ACCAGCGCT	TAGCGCCGCA	GTCAGGCCA	AGAAAGCCGT	CGAACGAAAT	GGCATGTTGC	360
TGCAGCAGAA	GATCGCCGAG	CGAACGAAACG	TGCTCAGCCA	GCTCGAGCAG	GCGAAGATGC	420
AGGAGCAGGT	CAGCCCTACG	TGCGGTGCA	TGAGTGAAGCT	CGCCGCGCCA	GGCAACACCG	480
CGAGCCTCGA	CGAGGTGCGC	GACAAGATCG	AGCGTCGCTA	CGCCAAACGCG	ATCGGTTCCG	540
CTGAACCTTG	CGAGAGT					557

## (2) INFORMATION FOR SEQ ID NO:222:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

CAGGATAGGT	TTCGACATCC	ACCTGGGTT	CGCACCCCGT	GCGCGACCGT	GTGATAGGCC	60
AGAGGGTGCAC	CTGCGCCGAC	CGACGATCGA	TGCGAGGAGTC	AACAGAAATG	GCCTTCTCCG	120
TCCAGATCGG	GGCAGCTCGGT	GAGAGCGTC	CCGAGGGGAC	GGTTACCCG	TGGCTCAAAC	180
AGGAAGGCGA	CACGGTCGAA	CTCGACGAGC	CCCTCGTGGGA	GGT		223

## (2) INFORMATION FOR SEQ ID NO:223:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

AAGAAAGTACA	TCTGCCGGTC	GATGTCGGCG	AACCACCGCA	GCCAACCGGC	GCGTAGCCG	60
ACCAGGACCA	CCGCATAACG	CCAGTCGGG	CGCACAAACA	TACGCCACCC	CGCGTATGCC	120
AGGACTGGCA	CCGCCACGCC	CCACATCGCC	GGGCTGCGGA	CCAGCATCTC	GGCCTTGGAG	180
CACGACTGTG	CGCCCGACCC	TGCAACGCTCT	TGCTGGTCA	TGGCGTACAG	CACCGCCCGC	240
AACGACATGG	GGCAGGTCCA	CGGTTGGAT	TCCCAAGGGT	GGTAGTTGCC	TGCGGAATTC	300
GTCAGACATGG	CGTGGAACTG	GAACGCTTTC	GGCGGTATT	GGCAGAGGCC	GCGCACCGGC	360
TGGGGCAGGG	GAACAAACCGA	GTGGCGACCG	ACCGCTTGCAC	CGCACCGCATG	CGGATGATC	420
CGGGTCTCGG	ACGCGAACCA	CGGAGCGTAG	GTGGGCAAGAT	AGACCGCGAA	CGGGATCAAC	480
CCGAGCGAT	ACCCGCTGGG	AAGCACGTC	CGCCGCACTG	TTCCCAAGCCA	CGGTCTTGC	540
ACTTGGTATG	AACTGCGCGC	CGCCACGTC	ACGCCAGC			578

## (2) INFORMATION FOR SEQ ID NO:224:

205220-Eth8h300T

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

ACAACGATCG	ATTGATATCG	ATGAGAGACG	GAGGAATCGT	GGCCCTTCCC	CAGTTGACCG	60
ACGAGCAGCG	CGCCGCGCCG	TTGGAGAGG	CTGCTGCGC	ACGTGAGGG	CGAGCAGAGC	120
TCAAGGATCG	GCTCAAGCGT	GGCCGACCA	ACCTCACCA	GGTCCTCAAG	GACGCGGAGA	180
GCGATGAGT	CTTGGGCAA	ATGAAGGTGT	CTGCGCTGT	TGAGGCTTG	CCAAAGGTTGG	240
GCAAGGCTAA	GGCCGAGGAG	ATCATGACCG	AGCTGGAAAT	TGCGCCCCAC	CCCGCCGCT	300
TCGTTGGCTC	GGTGGACCGTC	AGCGCAAGGC	CCTGCTGGAA	AAAGTTCGGCT	CCGGCTTAACC	360
CCGGCGGGCG	ACGATGGGGG	CCGGAAGGGC	TGTTGGTGGC	GTACCCCCC	ATACGGGGGA	420
GAAGGGGCT	GACAGGGCA	GCTCACAAATT	CAGGCCAAC	GGCCCGGTGG	GGGGGAACCC	480
GC						484

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

AGGACTGGCA	CCGCCAGGCCA	CCACATCGCG	GGCGTGGCGA	CCAGCATCTC	GGCCTTGAAC	60
CACGACTGTG	CGCCGCAGCC	TGCAACGCTC	TGCTGGTCGA	TGGCGTACAG	CACCGCCCGC	120
AACGACATGG	GCCAGGTCGA	CGGTTTGAT	TCCCAAGGGT	GGTAGTTGCC	TGCGGAATTG	180
GTCAGGCCCG	CCTGGAAGTG	GAACGCTTGTG	CCGGTGTAGT	GGCAGAGCGA	GGCGACGGGG	240
TCGGGCAGCG	AAACAAACCGA	GGTGCACCG	ACCGCTTGAC	CGAGCGCATG	CGGATCGATC	300
GCGGCTCGG	ACCGGAACCA	CGGAGCTAG	GTGGCCAGAT	AGACCCGCAA	CGGGATCAC	360
CCCAAGCGAT	ACCGCTGGG	AAAGCACCTCA	CGCCGACTG	TCCCCAGCCA	CGGTCTTTGC	420
ACTTGGTACT	GACGTCGCGC	CGCCACGTCG	AAAGCCAGCG	CCATCGCGCC	GAAGAACAGC	480
ACGAAGTACA	CGGCCAGCCA	CTTGGTGGCG	CAAGCCAACT	CCAAGCAGCA	CCCCGGC	537

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Gly Gly Ala Ala Ala Gly Gln Ser Asp Val His Pro Phe Ala Asn  
 1 5 10 15  
 Leu Ile Ala Val Asp Asp Glu Arg Ala Glu Arg Arg Asp Asp Glu Glu  
 20 25 30  
 Arg Gln Glu Ala Val Gln Gln Arg Gly Pro Arg Gly Asp Glu Ala Asp  
 35 40 45  
 Pro Val Ala Asp Gln Gln His Pro Gly Asp Gly Ala Asp Gln Cys Arg  
 50 55 60  
 Pro Ala Asp Pro Pro His Asp Pro His His Gln Arg His Gln Asp His  
 65 70 75 80  
 Thr Gln Gln Gly Ala Gly Glu Pro Pro Ala Glu Ser Val Val Thr Glu  
 85 90 95  
 Asp Gly Leu Pro Asp Arg Asp Gln Leu Leu Thr Asp Arg Arg Val Asn  
 100 105 110  
 His Gln Ala Val Pro Gly Val Val Phe His Pro Met Val Val Gln His  
 115 120 125  
 Leu Pro Gly Leu Ala Val Arg  
 130 135

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

Gln Lys Tyr Gly Gly Ser Ser Val Ala Asp Ala Glu Arg Ile Arg Arg  
 1 5 10 15  
 Val Ala Glu Arg Ile Val Ala Thr Lys Lys Gln Gly Asn Asp Val Val  
 20 25 30  
 Val Val Val Ser Ala Met Gly Asp Thr Thr Asp Asp Leu Leu Asp Leu  
 35 40 45  
 Ala Gln Gln Val Cys Pro Ala Pro Pro Pro Arg Glu Leu Asp Met Leu  
 50 55 60  
 Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu Val Ala Met Ala Ile  
 65 70 75 80  
 Glu Ser Leu Gly Ala His Ala Arg Ser Phe Thr Gly Ser Gln Ala Gly  
 85 90 95  
 Val Ile Thr Thr Gly Thr His Gly Asn Ala Lys Ile Ile Asp Val Thr  
 100 105 110  
 Pro Gly Arg Leu Gln Thr Ala Leu Glu Glu Gly Arg Val Val Leu Val  
 115 120 125  
 Ala Gly Phe Gln Gly Val Ser Gln Asp Thr Lys Asp Val Thr Thr Leu  
 130 135 140  
 Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala Met  
 145 150 155

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

205230-E184740000

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

Pro Ala Tyr Pro Ala Gly Thr Asn Asn Asp Arg Leu Ile Ser Met Arg  
 1 5 10 15  
 Asp Gly Gly Ile Val Ala Leu Pro Gln Leu Thr Asp Glu Gln Arg Ala  
 20 25 30  
 Ala Ala Leu Glu Lys Ala Ala Ala Arg Arg Ala Arg Ala Glu Leu  
 35 40 45  
 Lys Asp Arg Leu Lys Arg Gly Gly Thr Asn Leu Thr Gln Val Leu Lys  
 50 55 60  
 Asp Ala Glu Ser Asp Glu Val Leu Gly Lys Met Lys Val Ser Ala Leu  
 65 70 75 80  
 Leu Glu Ala Leu Pro Lys Val Gly Lys Val Gln Ala  
 85 90

(2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

Thr Val Glu Leu Asp Glu Pro Leu Val Glu Val Ser Thr Asp Lys Val  
 1 5 10 15  
 Asp Thr Glu Ile Pro Ser Pro Ala Ala Gly Val Leu Thr Lys Ile Ile  
 20 25 30  
 Ala Gln Glu Asp Asp Thr Val Glu Val Gly Gly Glu Leu Ser Val Ile  
 35 40 45  
 Gly Asp Ala His Asp Ala Gly Glu Ala Ala Val Pro Ala Pro Gln Lys  
 50 55 60  
 Val Ser Ala Gly Pro Thr Arg Ile  
 65 70

(2) INFORMATION FOR SEQ ID NO:230:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10084843 22502

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

Ala	Ala	Asp	Ile	Gly	Ala	Ala	Pro	Ala	Pro	Lys	Pro	Ala	Pro	Lys	Pro
1			5				10			15					
Val	Pro	Glu	Pro	Ala	Pro	Thr	Pro	Lys	Ala	Glu	Pro	Ala	Pro	Ser	Pro
	20					25					30				
Pro	Ala	Ala	Gln	Pro	Ala	Gly	Ala	Ala	Glu	Gly	Ala	Pro	Tyr	Val	Thr
	35					40				45					
Pro	Leu	Val	Arg	Lys	Leu	Ala	Ser	Glu	Asn	Asn	Ile	Asp	Leu	Ala	Gly
	50					55			60						
Val	Thr	Gly	Thr	Gly	Val	Gly	Gly	Arg	Ile	Arg	Lys	Gln	Asp	Val	Leu
65			70				75			80					
Ala	Ala	Ala	Glu	Gln	Lys	Lys	Arg	Ala	Lys	Ala	Pro	Ala	Pro	Ala	Ala
	85					90				95					
Gln	Ala	Ala	Ala	Ala	Pro	Ala	Pro	Lys	Ala	Pro	Pro	Glu	Asp	Pro	Met
	100					105						110			
Pro															

## (2) INFORMATION FOR SEQ ID NO:231:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

Val	Leu	Val	Ser	Ile	Ser	Ala	Asp	Glu	Asp	Ala	Thr	Val	Pro	Val	Gly
1			5			10		15							
Gly	Glu	Leu	Ala	Arg	Ile	Gly	Val	Ala	Ala	Asp	Ile	Gly	Ala	Ala	Pro
	20				25					30					
Ala	Pro	Lys	Pro	Ala	Pro	Lys	Pro	Val	Pro	Glu	Pro	Ala	Pro	Thr	Pro
	35				40					45					
Lys	Ala	Glu	Pro	Ala	Pro	Ser	Pro	Pro	Ala	Ala	Gln	Pro	Ala	Gly	Ala
	50				55				60						
Ala	Glu	Gly	Ala	Pro	Tyr	Val	Thr	Pro	Leu	Val	Arg	Lys	Leu	Ala	Ser
65					70				75			80			
Glu	Asn	Asn	Ile	Asp	Leu	Ala	Gly	Val	Thr	Gly	Thr	Gly	Val	Gly	Gly
	85				90					95					
Arg	Ile	Arg	Lys	Gln	Asp	Val	Leu	Ala	Ala	Glu	Gln	Lys	Lys	Arg	
	100				105					110					
Ala	Lys	Ala	Pro	Ala	Pro										
	115														

## (2) INFORMATION FOR SEQ ID NO:232:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

Asp	Pro	Lys	Val	Gln	Ile	Gln	Gln	Ala	Ile	Glu	Glu	Ala	Gln	Arg	Thr
1				5					10				15		
His	Gln	Ala	Leu	Thr	Gln	Gln	Ala	Ala	Gln	Val	Ile	Gly	Asn	Gln	Arg
								20		25			30		
Gln	Leu	Glu	Met	Arg	Leu	Asn	Arg	Gln	Leu	Ala	Asp	Ile	Glu	Lys	Leu
								35		40		45			
Gln	Val	Asn	Val	Arg	Gln	Ala	Leu	Thr	Leu	Ala	Asp	Gln	Ala	Thr	Ala
								50		55		60			
Ala	Gly	Asp	Ala	Ala	Lys	Ala	Thr	Glu	Tyr	Asn	Asn	Ala	Ala	Glu	Ala
								65		70		75		80	
Phe	Ala	Ala	Gln	Leu	Val	Thr	Ala	Glu	Gln	Ser	Val	Glu	Asp	Leu	Lys
								85		90		95			
Thr	Leu	His	Asp	Gln	Ala	Leu	Ser	Ala	Ala	Gln	Ala	Lys	Lys	Ala	
								100		105		110			
Val	Glu	Arg	Asn	Ala	Met	Val	Leu	Gln	Gln	Lys	Ile	Ala	Glu	Arg	Thr
								115		120		125			
Lys	Leu	Leu	Ser	Gln	Leu	Glu	Gln	Ala	Lys	Met	Gln	Glu	Gln	Val	Ser
								130		135		140			
Ala	Ser	Leu	Arg	Ser	Met	Ser	Glu	Leu	Ala	Ala	Pro	Gly	Asn	Thr	Pro
								145		150		155		160	
Ser	Leu	Asp	Glu	Val	Arg	Asp	Lys	Ile	Glu	Arg	Arg	Tyr	Ala	Asn	Ala
								165		170		175			
Ile	Gly	Ser	Ala	Glu	Leu	Ala	Glu	Ser							
								180		185					

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

Val	Ser	Thr	Ser	Thr	Trp	Val	Pro	His	Pro	Val	Arg	Asp	Arg	Val	Ile
1					5			10			15				
Gly	Gln	Arg	Trp	Thr	Cys	Ala	Asp	Arg	Arg	Ser	Ile	Glu	Ser	Thr	
					20			25			30				
Glu	Met	Ala	Phe	Ser	Val	Gln	Met	Pro	Ala	Leu	Gly	Glu	Ser	Val	Thr
					35			40			45				
Glu	Gly	Thr	Val	Thr	Arg	Trp	Leu	Lys	Gln	Glu	Gly	Asp	Thr	Val	Glu
					50			55			60				
Leu	Asp	Glu	Pro	Leu	Val	Glu									
					65			70							

(2) INFORMATION FOR SEQ ID NO:234:

10084845-022603

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

Glu Val His Leu Pro Val Asp Val Gly Glu Pro Arg Gln Pro Thr Gly  
 1 5 10 15  
 Ala Val Ala Asp Gln Asp His Arg Ile Thr Pro Val Pro Ala His Lys  
 20 25 30  
 His Thr Pro Pro Arg Val Cys Gln Asp Trp His Arg Gln Pro Pro His  
 35 40 45  
 Arg Gly Arg Ala Asp Gln His Leu Gly Leu Asp Ala Arg Leu Cys Ala  
 50 55 60  
 Ala Ala Cys Asn Val Leu Leu Val Asp Gly Val Gln His Arg Pro Gln  
 65 70 75 80  
 Arg His Gly Pro Gly Pro Arg Phe Gly Phe Pro Arg Val Val Val Ala  
 85 90 95  
 Cys Gly Ile Arg Gln Ala Arg Val Glu Val Glu Arg Phe Gly Val  
 100 105 110  
 Leu Pro Glu Arg Ala His Gly Val Gly Gln Arg Asn Asn Arg Val Ala  
 115 120 125  
 Thr Asp Arg Leu Thr Asp Arg Met Pro Ile Asp Arg Gly Leu Gly Arg  
 130 135 140  
 Glu Pro Arg Ser Val Gly Gly Gln Ile Asp Arg Glu Arg Asp Gln Pro  
 145 150 155 160  
 Gln Arg Ile Pro Ala Gly Lys His Val Thr Pro His Cys Ser Gln Pro  
 165 170 175  
 Arg Ser Leu His Leu Val  
 180

## (2) INFORMATION FOR SEQ ID NO:235:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

Asn Asp Arg Leu Ile Ser Met Arg Asp Gly Gly Ile Val Ala Leu Pro  
 1 5 10 15  
 Gln Leu Thr Asp Glu Gln Arg Ala Ala Leu Glu Lys Ala Ala Ala  
 20 25 30  
 Ala Arg Arg Ala Arg Ala Glu Leu Lys Asp Arg Leu Lys Arg Gly Gly  
 35 40 45  
 Thr Asn Leu Thr Gln Val Leu Lys Asp Ala Glu Ser Asp Glu Val Leu  
 50 55 60

Gly Lys Met Lys Val Ser Ala Leu Leu Glu Ala Leu Pro Lys Val Gly  
 65 70 75 80  
 Lys Val Lys Ala Gln Glu Ile Met Thr Glu Leu Glu Ile Ala Pro His  
     85 90 95  
 Pro Ala Ala Phe Val Ala Ser Val Thr Val Ser Ala Arg Pro Cys Trp  
     100 105 110  
 Lys Ser Ser Ala Pro Pro Asn Pro Ala Gly Arg Arg Cys Gly Pro Glu  
     115 120 125  
 Gly Leu Trp Trp Ala Tyr Pro Arg Ile Arg Gly Arg Ser Gly Leu Thr  
     130 135 140  
 Gly Pro Ala His Asn Ser Gly Arg Thr Pro Arg Trp Gly Gly Thr Arg  
 145 150 155 160

## (2) INFORMATION FOR SEQ ID NO:236:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

Asp Trp His Arg Gln Pro Pro His Arg Gly Arg Ala Asp Gln His Leu  
 1 5 10 15  
 Gly Leu Asp Ala Arg Leu Cys Ala Ala Ala Cys Asn Val Leu Leu Val  
     20 25 30  
 Asp Gly Val Gln His Arg Pro Gln Arg His Gly Pro Gly Pro Arg Phe  
     35 40 45  
 Gly Phe Pro Arg Val Val Val Ala Cys Gly Ile Arg Gln Ala Arg Val  
     50 55 60  
 Glu Val Glu Arg Phe Gly Gly Val Val Pro Glu Arg Ala His Gly Val  
     65 70 75 80  
 Gly Gln Arg Asn Asn Arg Val Ala Thr Asp Arg Leu Thr Asp Arg Met  
     85 90 95  
 Pro Ile Asp Arg Gly Leu Gly Arg Glu Pro Arg Ser Val Gly Gln  
     100 105 110  
 Ile Asp Arg Glu Arg Asp Gln Pro Gln Arg Ile Pro Ala Gly Lys His  
     115 120 125  
 Val Thr Pro His Cys Pro Gln Pro Arg Ser Leu His Leu Val Leu Thr  
     130 135 140  
 Ser Arg Arg His Val Glu Arg Gln Arg His Arg Ala Glu Glu Gln His  
     145 150 155 160  
 Glu Val His Ala Gly Pro Leu Gly Gly Ala Ser Gln Ser Gln Ala Ala  
     165 170 175  
 Pro Arg

## (2) INFORMATION FOR SEQ ID NO:237:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

ATGCCAAGCC GGTGCTGATG CCCGAGCTCG GCGAATCGGT GACCGAGGGG ACCGTCATTC  
 GTGGCTGAA GAAGATCGGG GATTGCGGTC AGGTTGACGA GCCACTCGTG GAGGTGTCCA  
 CCGACAAAGT GGACACCGAG ATCCCGTCCC CGGTGCGCTGG GGTCTTGGTC AGTATCAGCG  
 CCGCAGGAGA CGCCACCGCG CCCGTCGCGC GCGAGTTGGC CGGATCGGT GTCGCTGCCG  
 AGATCGCGC CGCGCCGCC CCCAAGCCCC C

60  
 120  
 180  
 240  
 271

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 89 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

Ala Lys Pro Val Leu Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly  
 1 5 10 15  
 Thr Val Ile Arg Trp Leu Lys Ile Gly Asp Ser Val Gln Val Asp  
 20 25 30  
 Glu Pro Leu Val Glu Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro  
 35 40 45  
 Ser Pro Val Ala Gly Val Leu Val Ser Ile Ser Ala Asp Glu Asp Ala  
 50 55 60  
 Thr Val Pro Val GLY Gly Glu Leu Ala Arg Ile Gly Val Ala Ala Glu  
 65 70 75 80  
 Ile Gly Ala Ala Pro Ala Pro Lys Pro  
 85

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 107 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

GAGGTAGCGGG ATGGCCGGAG GAGCACCCCA GGACCGCGCC CGAACCGGG GTGCCGGTCA  
 TCGATATGTG GGCACCGTTC GTTCCGTCGG CCGAGGTAT TGACGAT

60  
 107

(2) INFORMATION FOR SEQ ID NO:240:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

ATGAAGTTGA AGTTTGCTCG CCTGAGTACTG GCGATACTGG TTGTCGCAGC GGCCTTGTG	60
TTTCTCGCT CGGGTGCAG CGCAGATCCA CCTGACCCGC ATCAGCCGAA CATGACGAAA	120
GGCTATTGCGC CGGGTGCAGC ATGGGGTTTG GGGGACTTGG CGGTGTGCGA CGGGGAGAAG	180
TACCCCGACG GCTCGTTTG GCACCACTGG ATGCAAACTG GTTTACCGG CCCACAGTTT	240
TACTTCGATT GTGTCAGCGG CGGTGAGCCC CTCCCCGGCC CGCCGCCACC GGGTGGTTGC	300
GGTGGGGCAA TTCCGTCCGA GCAGCCAAAC GCTCCCTGA	339

## (2) INFORMATION FOR SEQ ID NO:241:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Met Lys Leu Lys Phe Ala Arg Leu Ser Thr Ala Ile Leu Gly Cys Ala	
1 5 10 15	
Ala Ala Leu Val Phe Pro Ala Ser Val Ala Ser Ala Asp Pro Pro Asp	
20 25 30	
Pro His Gln Pro Asp Met Thr Lys Gly Tyr Cys Pro Gly Gly Arg Trp	
35 40 45	
Gly Phe Gly Asp Leu Ala Val Cys Asp Gly Glu Lys Tyr Pro Asp Gly	
50 55 60	
Ser Phe Trp His Gln Trp Met Gln Thr Trp Phe Thr Gly Pro Gln Phe	
65 70 75 80	
Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro Leu Pro Gly Pro Pro Pro	
85 90 95	
Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser Glu Gln Pro Asn Ala Pro	
100 105 110	

## (2) INFORMATION FOR SEQ ID NO:242:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

GTGACCACGG	TGGGCCCTGCC	ACCAACCCGG	GCAGCGGGCAG	CCGCGGCGGC	GCGGGCGGCT	60
CCGGCGGCAA	CGGTGGCGCC	GGGGGTAACG	CCACCGGCTC	AGCGGGCAAG	GGCGGCGCCG	120
GTGGAATGG	CGGTGATGGG	AGCTTCCGGG	CTACCCAGGG	CCCGGCTCC	ATCGGGGTC	180
CGGGCGGCC	CGGCGGCAAC	GGCGGCAAGG	GGCGGCGCCG	TGGCAGCAAC	CCCAACGGCT	240
CAGGTGGCGA	CGGCGGCAA	GGCGGCAAGC	GCCTGGCCGG	CGGCAACGGG	GGCTCGATCG	300
GGCCCAACAG	CGGCATCGTC	GGCGGTTCCG	GTGGGGCGGG	TGGCGCTGGC	GGCGGCCGGC	360
GAACACGGC	C					371

## (2) INFORMATION FOR SEQ ID NO:243:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

GTCCGGGTCC	CACCAACGGG	CGGGCGGCC	CCTAGCGGCC	GGGGCACCCA	GCCCCCTTTTC	60
TTGACTCTGT	CAAGAAGG	GCCTTCTGT	TGGCTGGCCA	TGTTGGCATG	ATCGTGACCC	120
ATGGGCAACA	TGCGACTCGCA	CATCTCGGCC	AAGGTCTAGC	TCCATGGAA	TCGCGGCCG	180
GGTGGTGGAGC	ATCGGTCTAG	CGGTCTAGC	AGGGTTCCGG	GTACCTGTG	CCGACGCCACA	240
CCCCTGGGAG	GGGTTGGGTTG	TGGCTCTAGC	GGTGTCTGG	AAGGGGTCTGG	TCGGCAACAT	300
CGTGGGGCGG	CCAATGGGTTG	GGGTGGCGGT	GGTGTCTGG	GGTGTCTGG	TCGGCAACAT	360
CGAACTACCG	GGGTGCAACA	ACTGGGTGGA	CATCGGGCTG	CCCGAGGTGT	ACGACGATCC	420
CGAC						424

## (2) INFORMATION FOR SEQ ID NO:244:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

GCGATGGCGG	CCGGGGGTAC	CACCGCCAAT	GTGGAACGGT	TTCCCAACCC	CAACGATCCT	60
TTGCATCTGG	CGTCAATTGA	CTTCAGCCG	GCGGATTTCG	TCACCGAGGG	CCACCGTCTA	120
AGGGCGGATG	CGATCTTACT	GGGCCGTAAC	GACCGGCTGC	CTTTCGCGGA	GCCGCCGGAT	180
TGGGACTCTGG	TGGGACTCTGG	GGGCCGTAAC	ACCGGTCACCG	CCGACACGGT	GCGCATCGAC	240
GTCATCGCCG	ACGATATGCG	TCCCGAACTG	GGCGGGCGGT	CCAAACTCAC	CAGATCGCTC	300
CGGCTCTAGC	ATTGCGT					317

## (2) INFORMATION FOR SEQ ID NO:245:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

TGGCGTATGC	GCTTCGCAGC	CGGTGCCGCG	TCAACGCGCC	GGAGGCAATC	GCTTCGCTGC	60
CGAGGAATGG	TTCGATCACG	ATCCGACTGT	GCCGTCCTGC	ACCGACACCG	CCGTCCAACG	120
TGAACTGAGG	GGCGGAAATC	GGCGGAAATC	TGCCCCCTAG	TTCACGCTCG	GCGCTAACG	180
GTTCCTGGAA	TTGGGTGGCG	GCTCTCGGC	GAACGCCGCG	GGGCCCTTCCT	TGGCTCGTC	240
GGACAGGAAG	TGCGATGATG	CGATCTGGGT	GTCGATCTGGT	AAACGCCCTCGT	TTTCGGGCAT	300
GCACCTGGTC	TGCGGGATGG	ACCGCAAGAT	GGCCTGCACG	GGCCAGGGGTG	CCTTACGGCGA	360
GATGGCGTGC	GCAAGTTCTA	GAACCTTGGT	CAACGCCCTGG	CCGTCGGGCA	CACGTGGCCG	420
AT						422

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

GCGTGCCTG	GAACACAGC	CCGGGGCTGC	CAGATCTCCC	GGACTCGGT	GTGCCCCCGG	60
TGGCGTCGTT	GCTCTCTGA	CGGGCGCGG	CGACCATAGA	GTCGCTAATG	CCCAGGTAGC	120
GGCCCGAGGT	CATGGAGTGC	ATGATGATGC	GACTCTCCAG	CTGCGGACCC	GGGAGCTTGC	180
CATCGGCGCT	GATCAGCCAG	GACCGCTGAG	ACAAGTCCGT	CGAAATGCATA	GTGGCTTCCA	240
GAGTGGCCGT	GCCACTTCCG	GGCGTGTCTCA	CGGCAAATGC	CTTGATTTCT	AGCTCCGGCT	300
AGTGTCCTCG	CATGCCCTGC	GGGGATGAATG	GGAAACCGCAG	GATGGGGACA	AACGGGCTCG	360
ACCTCAGGTT	TGCGCTTTC	CGCACAGTGG	TCGACAGCCG	GTACTCGGCA	AAAATGCTGG	420
CCCCGA						426

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

AGACCGGGCGA	GGGTGTGGTC	GCTGCCCGCG	GCATTGTCGA	TAATCTGCGC	TGGGTCGACG	60
CGCGGATCAA	CTAGTGAGGC	GCAACGCTAG	GCTTGGGAT	ACCCACAGCT	AAAAAGTTTA	120
TCAAAGAAC	GAAGAAGGTT	GCCATGAGCA	CTGTTGCCGC	CTACGCCGCC	ATGTCGGCGA	180
CCGAACCCCT	GACCAAGACC	ACGATCACCC	GTCGCGACCC	GGGCCCGCAC	GACATGGCGA	240
TCGACATCAA	ATTCGGCGGA	ATCTGTCGCT	CGGACATCCA	TACCGTCAA	ACCGAATGGG	300
GGCAACCGAA	TTTACCTGTG	GTCCCTG				327

## (2) INFORMATION FOR SEQ ID NO:248:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

Asp	His	Gly	Gly	Pro	Ala	Thr	Asn	Pro	Gly	Ser	Gly	Ser	Arg	Gly	Gly
1															
														15	
Ala	Gly	Gly	Ser	Gly	Gly	Asn	Gly	Gly	Ala	Gly	Gly	Asn	Ala	Thr	Gly
20															
														30	
Ser	Gly	Gly	Lys	Gly	Gly	Ala	Gly	Gly	Asn	Gly	Gly	Asp	Gly	Ser	Phe
35															
														45	
Gly	Ala	Thr	Ser	Gly	Pro	Ala	Ser	Ile	Gly	Val	Thr	Gly	Ala	Pro	Gly
50															
														60	
Gly	Asn	Gly	Gly	Lys	Gly	Gly	Ala	Gly	Gly	Ser	Asn	Pro	Asn	Gly	Ser
65															80
Gly	Gly	Asp	Gly	Gly	Lys	Gly	Gly	Asn	Gly	Gly	Ala	Gly	Gly	Asn	Gly
85															95
Gly	Ser	Ile	Gly	Ala	Asn	Ser	Gly	Ile	Val	Gly	Ser	Gly	Gly	Ala	
100															110
Gly	Gly	Ala	Gly	Gly	Ala	Gly	Gly	Asn	Gly	Ser					
115															

## (2) INFORMATION FOR SEQ ID NO:249:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

Met	Ala	Ala	Ala	Gly	Thr	Thr	Ala	Asn	Val	Glu	Arg	Phe	Pro	Asn	Pro
1															15
Asn	Asp	Pro	Leu	His	Leu	Ala	Ser	Ile	Asp	Phe	Ser	Pro	Ala	Asp	Phe
20															
															30
Val	Thr	Glu	Gly	His	Arg	Leu	Arg	Ala	Asp	Ala	Ile	Leu	Arg	Arg	
35															45
Thr	Asp	Arg	Leu	Pro	Phe	Ala	Glu	Pro	Pro	Asp	Trp	Asp	Leu	Val	Glu
50															
															60
Ser	Gln	Leu	Arg	Thr	Thr	Val	Thr	Ala	Asp	Thr	Val	Arg	Ile	Asp	Val
65															80
Ile	Ala	Asp	Asp	Met	Arg	Pro	Glu	Leu	Ala	Ala	Ala	Ser	Lys	Leu	Thr
85															95
Glu	Ser	Leu	Arg	Leu	Tyr	Asp	Ser								
100															

## (2) INFORMATION FOR SEQ ID NO:250:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

Ala	Tyr	Ala	Leu	Arg	Ser	Arg	Cys	Arg	Val	Asn	Ala	Pro	Glu	Ala	Ile
1			5					10					15		
Ala	Ser	Leu	Pro	Arg	Asn	Gly	Ser	Ile	Thr	Ile	Ala	Val	Cys	Arg	Arg
			20					25					30		
Ala	Pro	Thr	Pro	Pro	Ser	Asn	Val	Asn							
			35					40							

## (2) INFORMATION FOR SEQ ID NO:251:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

Val	Pro	Leu	Asn	Thr	Ser	Pro	Arg	Leu	Pro	Asp	Leu	Pro	Asp	Ser	Val
1				5				10					15		
Val	Pro	Pro	Val	Ala	Ser	Leu	Leu	Ser							
			20					25							

## (2) INFORMATION FOR SEQ ID NO:252:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

Met	Ser	Thr	Val	Ala	Ala	Tyr	Ala	Ala	Met	Ser	Ala	Thr	Glu	Pro	Leu
1				5					10				15		
Thr	Lys	Thr	Thr	Ile	Thr	Arg	Arg	Asp	Pro	Gly	Pro	His	Asp	Met	Ala
				20				25					30		
Ile	Asp	Ile	Lys	Phe	Ala	Gly	Ile	Cys	Arg	Ser	Asp	Ile	His	Thr	Val
			35					40					45		

10084842 202200 20084842

Gln Thr Glu Trp Gly Gln Pro Asn Leu Pro Val Val Pro  
 50 55 60

## (2) INFORMATION FOR SEQ ID NO:253:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

GCTTGGAGCC	CTGGAGCGAC	GGTGTGGGTC	TGGGGTCTGA	TTCGTTCTCG	GCGAAGTCA	60
ACTAAAGACC	ACGTTGACAC	CCAAACCGCG	GCCCCGATG	GGCCGTCGG	GCGTAGAACG	120
TTTGACCGCG	GCGCAGAACG	TTCGCTGCTG	CGGCCCATGC	AGATCGCACA	CGCTTGCCTG	180
ACACATCGGT	GGAGCCGTG	GTAAACGCCAG	GCT			213

## (2) INFORMATION FOR SEQ ID NO:254:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

CCGAGCTGCT	GTTCGGGGCC	GGCGGTGCGG	GCGGCGCGGG	TGGGGCGGGC	ACCGACGGCG	60
GGCCCGGTGC	TACCGGGCGG	ACCGGGGAC	ACCGCGGAGT	CGCGCGGAC	GGCGGATGGC	120
TGGCACCCGG	CGGGGCGCGC	GGGGCGCGCG	GGCAAGCGG	GGCAGGTGGT	GCCCCGAGCG	180
ATGGTGGCGC	GTTGGGTGCT	ACCGGGCGGA	CGGGCGGTAC	CGGCAGCGCC	GGTGGCGCCG	240
GCGGTCGGG	CAACACTCTG	CTGGGGCTG	GGGGACAGGG	CGGCCTCGGC	GGCGCCGGCG	300
GACAAGGGG	CACCGGGCGG	GGCGCGGGA	GATGGCTTC	TGGGGGTGT	CAGTGGCACT	360
GGTGGTA						367

## (2) INFORMATION FOR SEQ ID NO:255:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

AAGGCGTGAT	TGGCAAGGCG	ACCGCGCAGC	GGCCCGTAGC	C CGGGGACGG	CCCAGGCC	60
GACCGCGACG	GCCGGTGCT	GACCGGGTCA	GCGACCGAGC	GCGCTGACCG	TGCGCGCTCGT	120
CTACTTCGAC	GCCAGCGCCT	TCGTCAAACT	TCTCACCACC	GAGACAGGGA	GCTCGCTGGC	180

GTCCGCTCTA	TGGGACGGGT	GGGACGGCG	ATTGCTTCAAC	CGCCTGGCCT	ACCCCGAAGT	240
CCGGCGCCGA	CTCGCTGCAA	CGGGCCCAA	TCACGACTTA	ACCGAATCCG	AGCTCGCCGA	300
CGCCGAGGGT	GACTGGGAGG	ACTTCTGGC	CGCACCCGCC	CACTCGAACT	CACCGCGAGC	360
GTTGACACGC	ACGCCGGGCA	CCTCGCCCGA	ACACATGCGCT	TACCGGGAGC	CGACACCGTT	420

## (2) INFORMATION FOR SEQ ID NO:256:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

CTCTTGTGG	TGGCATCGGG	GGTACCCGGC	GAACCGGGG	CAACGCCGGT	ATGCTCGCCG	60
GGCGCCGGCG	GGCGCGGGGT	GGCGCGGGGT	TCAGCTTCAG	CACTGCCGGT	GGGGCTGGCG	120
GGCGCCGGCG	GGCGCGGGGG	CTGTTTACCA	CCGGCGGTGT	CGCGCCGCC	GGTGGGCAGG	180
GTCACACGGG	CGGGGGGGG	GGCGCCGGCG	GGGCCGGCGG	GTTGTTGGT	GCCGGCGGCA	240
TGGCGGGGGC	GGGGGATTC	GGGGATCACG	GAACGCTCGG	CACCGGGGGG	GCCGGCGGG	299

## (2) INFORMATION FOR SEQ ID NO:257:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

Leu	Glu	Pro	Trp	Ser	Asp	Gly	Val	Gly	Leu	Gly	Val	Asp	Ser	Phe	Ser	
1							5							10		15
Ala	Lys	Val		Asn												20

## (2) INFORMATION FOR SEQ ID NO:258:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

Glu	Leu	Leu	Phe	Gly	Ala	Gly	Ala	Gly	Ala	Gly	Ala	Gly
1							5					
Thr	Asp	Gly	Gly	Pro	Gly	Ala	Thr	Gly	Thr	Gly	Gly	His

20	25	30														
Val	Gly	Gly	Asp	Gly	Gly	Trp	Leu	Ala	Pro	Gly	Gly	Ala	Gly	Gly	Ala	
35							40					45				
Gly	Gly	Gln	Gly	Gly	Gly	Ala	Gly	Gly	Ala	Arg	Ser	Asp	Gly	Gly	Ala	Leu
50						55				60						
Gly	Gly	Thr	Gly	Gly	Thr	Gly	Gly	Thr	Gly	Gly	Ala	Gly	Gly	Ala	Gly	
65						70			75			80				
Gly	Arg	Gly	Thr	Leu	Leu	Leu	Gly	Ala	Gly	Gly	Gln	Gly	Gly	Leu	Gly	
							85			90			95			
Gly	Ala	Gly	Gly	Gln	Gly	Gly	Thr	Gly	Gly	Gly	Arg	Arg	Arg	Trp	Arg	
							100			105			110			
Ser	Gly	Gly	Cys	Gln	Trp	His	Trp	Trp								
						115			120							

## (2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

Gly	Val	Ile	Gly	Lys	Ala	Thr	Ala	Gln	Arg	Pro	Val	Ala	Ala	Gly	Arg
1						5					10			15	
Pro	Arg	Pro	Arg	Pro	Gln	Arg	Pro	Val	Ser	Asp	Arg	Val	Ser	Asp	Gln
							20			25			30		
Arg	Arg														

## (2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

Leu	Val	Gly	Gly	Ile	Gly	Gly	Thr	Gly	Gly	Thr	Gly	Gly	Asn	Ala	Gly
1						5				10			15		
Met	Leu	Ala	Gly	Ala	Ala	Gly	Ala	Gly	Gly	Ala	Gly	Gly	Phe	Ser	Phe
							20			25			30		
Ser	Thr	Ala	Gly	Gly	Leu	Phe									
							35			40			45		
Thr	Thr	Gly	Gly	Val	Gly	Gly	Ala	Gly	Gly	Gly	Gly	Gly	His	Thr	Gly
							50			55			60		
Ala	Gly	Gly	Ala	Gly	Ala	Gly	Gly	Leu	Phe	Gly	Ala	Gly	Gly	Met	
							65			70			75		80

Gly Gly Ala Gly Gly Phe Gly Asp His Gly Thr Leu Gly Thr Gly Gly  
 85 90 95  
 Ala Gly Gly

## (2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 282 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

TCCTGTTTCG	CGCCGGCGGG	GTGGCGGTG	TTGGCGGTGA	CGGTGTTGGCA	TCCTGGCA	60
CGCCCGCCCG	CGGGCGCGGT	GGTGGCGCG	GGGCGCGTGG	GCTGTTCAAG	GTCGGTGGGG	120
CCGGCGGGCG	CGGGCGGAATC	GGATTGGTGC	GGAACAGCGG	TGCCGGGGGG	TCCGGCGGGT	180
CCGGCCCTGGT	CTGGGGCGAC	GGCGGTGCGG	GGCGCGGGGG	TGGGGTGGG	TCCACTACCG	240
GCCTGTCGG	CGGGGGGGGC	GGCAACGCCA	GCCTGCTGGT	AA		282

## (2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 415 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

CGGCACGAGC	CGTGCTACTG	GTCAACTGAT	GCCCTGATTG	TGACCTTCCC	GGCGCCGGAT	60
CAGTGCCTCT	CGAGGACCGAC	GTAATATTG	AAAACCAATC	CGGCCGCGGA	GGCGAGGATG	120
AATGCCACAC	CGGGCGCGAT	CAGCCACCGG	AGCCACAAAG	CGATGCCGAC	CGCTGCCAAC	180
GAGCCGGACA	ACGGCACCAT	GATGCCAC	CAGCTATTCG	GACTGAAGAA	TCCAAGTTCT	240
CCTGCGCCCGT	CCTGATTTCTG	AGCGCCTCG	TAGTCCCTCGG	GGCGGGAAATC	TAACGGGGG	300
GCCACAAACC	GGAAAGAAGGT	GGCGACGATC	AACGCCATGC	CGCCGGTGAG	CGCCAACGCA	360
ATGGTGCAG	CCCACTCGAC	ACCACCGGTG	GCGAACATCG	AGGTCAACAC	GGCGT	415

## (2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 373 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

TCACCGCGTG	AACGGTTCGT	AACACTGATA	CGTATGCTTG	TCAGCGAGCA	GATCAAGTCC	60
AGTCGGACCA	ATGCCAGGAG	ATCATCGGCT	AGGCTCACGG	TTTCGCTTGG	GACGAGACGG	120
TATTGAGTTTC	TGGCGTTGGA	CGGTCGGTGG	CGTGTGGGA	AGTCTGACGC	GGCATCAGAA	180
CGGTTGTCAA	TACCACTTCTT	TGGGGATAT	GGCCTATTG	GTGTCGTCGG	GCCGCTCCAC	240
CGGATCCCTT	TTCGAACGTT	GCGAAGGGC	GGTCAGTTA	CGGCTGTTC	ACTGCGCGCT	300
GGCGTAGCTG	CGCGGCCTCG	ATCGTTTGA	ACGTCATCGC	AATTCGGCGA	ATGGGTGAGT	360
ACCTGAGCGT	CCT					373

## (2) INFORMATION FOR SEQ ID NO:264:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

CCAAACCGGA	CAGGCGGGCA	GCGACGGTGTG	GAAGTTGCAC	CACGGTGCAC	GCTCCATGTA	60
GCCAAACGGT	CCCGCGGGCG	TAGACGACGAG	ATCCGTGGAT	CGCGCGTTTCG	GTGTCGTCGG	120
GGCCGAGTAC	CCCGCGGGCG	AACCCGACGG	ACCAAGCAA	CGCGATCGAT	ACCGGGATTCG	180
CCACTCGTGC	CGAATTTCGAG	CTCCGTCGAC	AAGCTTGGGG	CCGCACTCGA	ACCCGGGTGA	240
ATGATTGAGT	TTAAACCGCT	TAGCAATAAC	TAGCATAAC	CCTTGGGGCC	TCTAAACCGG	300
TCTTGTAGGGG	TTTTTGTGCTG	AAAGGAGGAA	CTATATCCGG	ATAACCTGGC	GTAGTAGCGA	360
AGAGGCCCGC	ACCGATGCC	CTTCCCAACA	GTTGCGCAGC	CTGAAATGGCG	AATGGACCGC	420
CCC						423

## (2) INFORMATION FOR SEQ ID NO:265:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

AGTGGCCAGC	CGGTCGGGCCA	ATGCACTCCAG	CTCCGGTAC	GTCAGCTGAC	CATCCGCCCA	60
ACTGACCCAGC	AGCGAGTCAG	GCTGTGCCG	AGCGATTTCG	GCGAACCGGG	TATGCACCGC	120
GGGTGCGCAC	GTGCTCACAT	CCGGCAGGCC	GGGTGCGGTC	GGATGCTGCT	CGCGCTCCAG	180
CAGAATGTCG	ACGTCGGCA	GGCGCCGATC	CCACCGGCTG	ACCAAGCGT	GTAACACAGC	240
CAGCACCCGC	CTGGCGAGGC	TTTCGGGGCG	CATCGTGGCC	AGCGCACCGT	CGAGCACCTC	300
CACTAGCAGC	GTGAGGCTAC	CGGTGCTGG	GTGCGGGGG	ACGGTCACCG	GAAAGTGCAG	360
CAAACCTCT	AGCGCCACCG	GACGGAAAGT	CACCCGGTTT	GCAGA		404

## (2) INFORMATION FOR SEQ ID NO:266:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

GTCTCTGGTCC	CAGGCTGTTTC	TTCGAACCCG	CTGGCTAACT	TCGCACCCGG	GTATCCGCC	60
ACCATCGAAC	CGCCCAAACC	GGCGGTGTC	CGGCCACTT	CGCAAGACCC	GGCGGGTGC	120
GTGCGACCA	TGAGCGGCCA	CCCCGGCG	GCACTATTG	ACAACGGAC	CGCCAATTG	180
GTGCGCTG	GGCCGGGCC	CGATTCGGG	GCACCCGCCA	GCATCATGGT	CTTCGATGAC	240
ATGCACGTTG	CACCGCGCT	CATTTTCTG	CGGGGCCCG	CAGCCGCGT	GACCAGGAC	300
GACCACGGCA	CGGCCCTTCCT	TGCCGCCCG	GGCGGTACT	TCGTTGGCGA	CCTGTCTCC	360
GGTCACACCG	CACGAGTGA	TGTCGCTGAC	GCAGCGCACA	CCGATTCAC	CGCGATCGCC	420
C						421

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

ATGCATATCA	CGCTCAACCC	CATCGCTGCT	GGGATCTCG	GGGCGGGGG	CAGTGAACTA	60
GACGAGCTG	GGCGCCCTAT	TCCGGCTG	GTCACGGCTG	GCTCGCGCT	GGCGGGCTA	120
CCGAAACCCA	AAACGCGACTA	TGGCCGCTT	AGCCCGTGGG	GCCGGCTGGC	CGAGTGGGG	180
CGCCGATACG	ACACTCTCAT	CGACGAGCTC	ATCGAAGGCC	AGCGGGCCGA	CCCGAACTTC	240
GCGGATCGGA	CGGACGTTTT	GGCGTTGATG	CTGGCGACGA	CTTACGACGA	CGGTTCCATC	300
ATGTCGCGCA	AGGACATTTG	CGACGAACTG	CTCACGCTG	TTGCCGCCGG	GCACGAAACC	360
ACGGCGGCCA	CATGGGCTGG	CGCTTCGAAC	GGCTCAACCG	GCACCCGAC	GTGCTCGGG	420
CTCTGG						426

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

GTCTCTGGTCC	CAGGCTGTTTC	TTCGAACCCG	CTGGCTAACT	TCGCACCCGG	GTATCCGCC	60
ACCATCGAAC	CGCCCAAACC	GGCGGTGTC	CGGCCACTT	CGCAAGACCC	GGCGGGTGC	120
GTGCGACCA	TGAGCGGCCA	CCCCGGCG	GCACTATTG	ACAACGGAC	CGCCAATTG	180
GTGCGCTG	GGCCGGGCC	CGATTCGGG	GCACCCGCCA	GCATCATGGT	CTTCGATGAC	240
GTGCACGTTG	CACCGCGCT	CATTTTCTG	CGGGGCCCG	CAGCCGCGT	GACCAGGAC	300
GACCACGGCA	CGGCCCTTCCT	TGCCGCCCG	GGCGGTACT	TCGTTGGCGA	CCTGTCTCC	360
GGTCACACCG	CACGAGTGA	TGTCGCTGAC	GCAGCGCACA	CCGATTCAC	CGCGATCGCC	420

CGCCGCTCCG ACGGCAAGCT GGTGCTGGGC AGCGCAGATG GCGCCGTCTA CACGCTTGCC	480
AAGAACCCGC AGTTGACCGG CGTCGGCGCC GCCACCGTAG CC	522

## (2) INFORMATION FOR SEQ ID NO:269:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 739 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

GCTGGGGCGC CGGCCTGGTC GGCAGCCCCA GCGCCCTGGC CCGAGACCCCG CGCAAACCCA	60
ACCCGTGGCC CTTAGTGGCC GGCAGCCCCA CGTCCTCGCT CGTCCTCGTG TTGGGGCGCCA	120
TCGGCATCTG GATCGCCATC CGGGCCAAAGC CGGTACAGCC GCCTCAGCGG TTGGGGAGGG	180
AGCGCCTTAG CGGCCCTACTG CTGAACTCTCT CAGAACTCAA CGCCGTGATG GGCTGCTCGT	240
CCATCGACGCC GGGCCAAACCC ATCACATCGA TGGACTCTTC GCGGGTGACG GTGTCCTGC	300
CGGACTGCCA GGGCGCGCTA TATACCGACG AGGATCGGTG ATATGCCGCC ACCGGCTACAA	360
CCGCCATCAA CGGCTTGAT TCATCCGAGC CGGGCGACAA CTACGAACAT TGGGTGAACC	420
AAGCGCTGT CGCCCTTCCG ACCGCGCAGCA AAGCCCGCAGC GTTCGTGCG ACTTCGGCCG	480
ACAAATGGA AAGCTGGCA GGCAGAGCGG TCACCGTCAC GAAATAAGGGC AAGACCTACCC	540
GGTGGACCTT CGCCGACCTC AAAGGCAGCC CGCCGACGAT CACGGTGATA GACACCCAAAG	600
AAGGGCGCTA GGGCTGGGAA TGCCAACCGC CGATGAGCGT GACCAACCAT GTGGTTGTGCG	660
ACGTCAACGC ATCGGGTACAGATCACCA ATCAAGCAGG CCAGATCGCC CGCAAGATCT	720
GTTGACAAAG TCAACAAAGG	739

## (2) INFORMATION FOR SEQ ID NO:270:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 69 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

AGACGTCGTC GAGGCCGCCA TCGCCCGCGC CGAAGCCGTT AACCCGGCAC TGAACGCGTT	60
GGCGTATGC	69

## (2) INFORMATION FOR SEQ ID NO:271:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 523 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

ACTGCACCCG	GCAGGGCGGA	CCAACGGATC	GGGTCAACTA	GCACTGCCGG	TGGAGGCC	60
CCCGCGGTCT	GTGCCCTTCCC	ACGGGGAAAC	CTTGGGCAGC	GCGGCTCCAG	AAGGGTTGGA	120
GGGAGAGTTG	GACGACCGTA	TGCGAGACGG	GTTCGGCGTC	TTCAAGCTCGG	CCAGTCTCGC	180
CGAAGGGCTG	CGGGGTCGGC	TGACCCCGAT	GACGCTGGAT	GTCCAGTTGA	GTGGACTGCG	240
CGCGGCCGGT	CGGGCGATGG	GTCGGGTACT	GGCGCTTGGC	GGTGTCTTGTG	CCGATGAGTG	300
GGAGAGAGAA	GCCATCGCGG	TGTCGGTATG	GGCCCGCTAT	ATCGGAGTGT	CGGCCAATAT	360
TGTGGCCGCC	GCCCCAACTCG	CGGGGTGGGA	CGCGCAGGGC	GTAACCCGGC	GGGCACTGGG	420
CGAGCAACCG	CAGGTCACTG	AGCTGCTTCC	GTTTGGTCGA	CCGCAACTTG	CGGGCGGACC	480
GTCGCGCTCG	GTCGGGAAGG	TGGTCGTGAC	GGCACGGTCG	CTG		523

## (2) INFORMATION FOR SEQ ID NO:272:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

GTGTGGGTGT	CGTCGGGTTA	GGAGCGACTT	CCCCGGCCGG	CGCCGGCGCC	GGAGCGGGCT	60
CTGAGGAAAC	CGGTGGCGGC	GCCGGCGGG	GGGGCGGATAA	AGGCGGGATC	GATTCGGCCA	120
GCCCCCTTGGC	CGCGCCCTTG	TCCACCGGGT	TGTTGGCGGT	CCCGAGCCAT	ACCACAAACC	180
AACGCTGAAG	GGGCCGGCG	TCCGGTGGT	TCGCGCGGG	CGAC		224

## (2) INFORMATION FOR SEQ ID NO:273:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

TGAACTGACT	GCCCCGCTCG	ATCGCGCGC	GGCGCGTGT	ATAGCTCGC	CGCAGGCCA	60
TGAACTGCTC	TTCGCCATAG	CGGGCTTGG	TCTCGCCCT	GTCCAAACCC	TGAGCGCGC	120
CGTAGTGGCG	TTCTGTGAGC	CGCAGCTAC	GCCGCACCGG	AATCCAGAGC	CGATCGCGCG	180
TGTCACACGC	CAGATCGCGG	GTGGTGATGC	CGCGCCGCG	CAACGGAGTG	TAGAGCACGT	240
CGGGCAATAG	GTCGTGTTCC	CGCATCAGCT	CGCGCTTCG	AAACCGCTCT	GCCTGGCCCT	300
TGTCGCTAG	GGCGACATCG	ACCCAGCGG	TGAACAGTTT	GAGGGCATTC	CAGTCGCTCT	360
CGCGTGGCG	CAGCAACACC	AGGCTGCCAG	TGTTTGCAT	ACCGGCAAGT	CTCTCACGCA	420
CTCCCGCACT	CCTCATCGTG	GACCAAAATG	CCCGAATTCT	CCTCGGTCCG	CTGCGCAGCG	480
CGTTCATACC	GGCGAGGTG	TGGCACCGT	AACGGCCGGT	T		521

## (2) INFORMATION FOR SEQ ID NO:274:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

CTCCAGGCTC ATTCTGCTCGA ACAAAAGCAC	CCGGCCGTAC AGCGGACGCC	CCCATTGTT	60
GTCGTGATAG TCCGCGTACA GCTGGGCATC	GGGCCCTGGA CGAACCTCCG	CCCAGGGGCA	120
GCGAACCCAGC CGCTCGCCCG	TCAGAACCGT AGTGCACGAC	AGTCTCGCCG	180
CGCGGAAGGGT TTGACCGCTC AGACTCGGCC	TCGGCGTCTT	CCGACGAGGC	240
CCGAGCTGAG AGCGTAGGCC	CTCGAGCTCA CGGCCGAGCC	GTTCCAGCAC	300
TGCGCTGGCT TGTTCGGCG	GTGAACTTGA CGCGCTCGAC	ATCGGGCGGG	360
GTGACCCCGA ACGCCCGCAG	CGTCTCGCC	CGCGCAAGGG	420
TCGCCA		CGGCAACTGC	426

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 219 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

GCGGACACGG CGGACAAAGC GCAATCGGCC	TCGGCGGGGG CGCCGGCGGC	GACGGGGGCC	60
AGGGCGGCC CGGGCCCGGA CTGTGGGTA	CTGGCGGCC	CGGGCGACAC	120
GGCGGTGGTA CGCGGCCCCC	ACCGCTGCC	GGTCAGGAG	180
GCGGGTGGGC	TGATCGGCA	GCATGGGCGC	219
CGGGCGGCC	CGGGCGGCC	CGGCGCGAC	

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 571 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

AAGATCATCG GGGCGCTCC TTAGCATCGC TGCCTCTGC ATCGTCCCG	GGCGGGATCA	60	
CGGAGGTCGG GCTTGTACCC CCACTCTCG AACGGTCAGC	ACACACTCG	120	
ATCCCTTTCG ACCTTGCCCC	GCAGACGCTG	GACATGCAG	180
TGGGTGCGCG TAACCCATA CCTGTCGAG	CAGCACATCA	CGAGTAAACA	240
CTTGGCGGCC AATGGCACCA ACAGGTCGAA	TTCCAGCGGT	GTCAACGAGA	300
GTGGCGATGTG ACCTTGTGCG CGGGTACGTC	GATTTCTACG	TCGGCGATGG	360
GGGGGGTTCG TCGCTGTGCG	CGGGTACGTC	ACAGCATCTC	420
CTTGAACCGC TTCACTGATGT AGTCGTCGGC	CGGCCGACCC	CGCGCAACCA	480
GGTGTGCGTC TTGGCGGTGA	GCATCACGAT	GGAACACCG	540
GCACACGTCG ATGCCGTCA	TACCGGGCA	GAATCGGCC	571

## (2) INFORMATION FOR SEQ ID NO:277:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

Leu Phe Gly Ala Gly Gly Val Gly Gly Val Gly Asp Gly Val Ala  
 1 5 10 15  
 Phe Leu Gly Thr Ala Pro Gly Gly Pro Gly Gly Ala Gly Gly Ala Gly  
 20 25 30  
 Gly Leu Phe Ser Val Gly Gly Ala Gly Gly Ala Gly Ile Gly Leu  
 35 40 45  
 Val Gly Asn Ser Gly Ala Gly Gly Ser Gly Gly Ser Ala Leu Leu Trp  
 50 55 60  
 Gly Asp Gly Gly Ala Gly Gly Ala Gly Val Gly Ser Thr Thr Gly  
 65 70 75 80  
 Gly Ala Gly Gly Ala Gly Gly Asn Ala Ser Leu Leu Val  
 85 90

## (2) INFORMATION FOR SEQ ID NO:278:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

Met Pro Pro Val Ser Ala Asn Ala Met Val Pro Ala His Ser Thr Pro  
 1 5 10 15  
 Pro Val Ala Asn Ile Glu Val Asn Thr Pro  
 20 25

## (2) INFORMATION FOR SEQ ID NO:279:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

205220 34848007

Lys Pro Asp Arg Pro Ala Ala Thr Val Gly Ser Cys Thr Thr Val Arg  
 1 5 10 15  
 Ala Pro Cys Ser Gln Pro Val Thr Thr Ala  
 20 25

## (2) INFORMATION FOR SEQ ID NO:280:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

Trp Pro Ala Gly Arg Pro Met His Pro Ala Pro Gly Thr Ser Ala Asp  
 1 5 10 15  
 His Pro Pro Asn  
 20

## (2) INFORMATION FOR SEQ ID NO:281:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

Val Leu Val Ala Gly Cys Ser Ser Asn Pro Leu Ala Asn Phe Ala Pro  
 1 5 10 15  
 Gly Tyr Pro Pro Thr Ile Glu Pro Ala Gln Pro Ala Val Ser Pro Pro  
 20 25 30  
 Thr Ser Gln Asp Pro Ala Gly Ala Val Arg Pro Leu Ser Gly His Pro  
 35 40 45  
 Arg Ala Ala Leu Phe Asp Asn Gly Thr Arg Gln Leu Val Ala Leu Arg  
 50 55 60  
 Pro Gly Ala Asp Ser Ala Ala Pro Ala Ser Ile Met Val Phe Asp Asp  
 65 70 75 80  
 Met His Val Ala Pro Arg Val Ile Phe Leu Pro Gly Pro Ala Ala Ala  
 85 90 95  
 Leu Thr Ser Asp Asp His Gly Thr Ala Phe Leu Ala Ala Arg Gly Gly  
 100 105 110  
 Tyr Phe Val Ala Asp Leu Ser Ser Gly His Thr Ala Arg Val Asn Val  
 115 120 125  
 Ala Asp Ala Ala His Thr Asp Phe Thr Ala Ile Ala  
 130 135 140

## (2) INFORMATION FOR SEQ ID NO:282:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

Met	His	Ile	Thr	Leu	Asn	Ala	Ile	Leu	Arg	Ala	Ile	Phe	Gly	Ala	Gly
1				5				10					15		
Gly	Ser	Glu	Leu	Asp	Glu	Leu	Arg	Arg	Leu	Ile	Pro	Pro	Trp	Val	Thr
				20				25					30		
Leu	Gly	Ser	Arg	Leu	Ala	Ala	Leu	Pro	Lys	Pro	Lys	Arg	Asp	Tyr	Gly
				35				40				45			
Arg	Leu	Ser	Pro	Trp	Gly	Arg	Leu	Ala	Glu	Trp	Arg	Arg	Gln	Tyr	Asp
				50				55			60				
Thr	Val	Ile	Asp	Glu	Leu	Ile	Glu	Ala	Glu	Arg	Ala	Asp	Pro	Asn	Phe
65					70				75					80	
Ala	Asp	Arg	Thr	Asp	Val	Leu	Ala	Leu	Met	Leu	Arg	Ser	Thr	Tyr	Asp
					85				90				95		
Asp	Gly	Ser	Ile	Met	Ser	Arg	Lys	Asp	Ile	Gly	Asp	Glu	Leu	Leu	Thr
				100				105					110		
Leu	Leu	Ala	Ala	Gly	His	Glu	Thr	Thr	Ala	Ala	Thr	Trp	Ala	Gly	Arg
				115				120				125			
Ser	Asn	Gly	Ser	Thr	Gly	Thr	Pro	Thr	Cys	Ser	Arg	Leu	Trp		
				130				135				140			

## (2) INFORMATION FOR SEQ ID NO:283:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

Val	Leu	Val	Ala	Gly	Cys	Ser	Ser	Asn	Pro	Leu	Ala	Asn	Phe	Ala	Pro
1					5			10					15		
Gly	Tyr	Pro	Pro	Thr	Ile	Glu	Pro	Ala	Gln	Pro	Ala	Val	Ser	Pro	Pro
					20			25					30		
Thr	Ser	Gln	Asp	Pro	Ala	Gly	Ala	Val	Arg	Pro	Leu	Ser	Gly	His	Pro
					35			40				45			
Arg	Ala	Ala	Leu	Phe	Asp	Asn	Gly	Thr	Arg	Gln	Leu	Val	Ala	Leu	Arg
				50			55				60				
Pro	Gly	Ala	Asp	Ser	Ala	Ala	Pro	Ala	Ser	Ile	Met	Val	Phe	Asp	Asp
65					70				75				80		
Val	His	Val	Ala	Pro	Arg	Val	Ile	Phe	Leu	Pro	Gly	Pro	Ala	Ala	Ala
					85			90				95			
Leu	Thr	Ser	Asp	Asp	His	Gly	Thr	Ala	Phe	Leu	Ala	Arg	Gly	Gly	
					100			105				110			

10032028480002

Tyr Phe Val Ala Asp Leu Ser Ser Gly His Thr Ala Arg Val Asn Val  
 115 120 125  
 Ala Asp Ala Ala His Thr Asp Phe Thr Ala Ile Ala Arg Arg Ser Asp  
 130 135 140  
 Gly Lys Leu Val Leu Gly Ser Ala Asp Gly Ala Val Tyr Thr Leu Ala  
 145 150 155 " 160  
 Lys Asn Pro

## (2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Trp Gly Ala Pro Pro Ser Gly Gly Pro Ser Pro Trp Ala Gln Thr Pro  
 1 5 10 15  
 Arg Lys Thr Asn Pro Trp Pro Leu Val Ala Gly Ala Ala Val Val  
 20 25 30  
 Leu Val Leu Val Leu Gly Ala Ile Gly Ile Trp Ile Ala Ile Arg Pro  
 35 40 45  
 Lys Pro Val Gln Pro Pro Gln Pro Val Ala Glu Glu Arg Leu Ser Ala  
 50 55 60  
 Leu Leu Leu Asn Ser Ser Glu Val Asn Ala Val Met Gly Ser Ser Ser  
 65 70 75 80  
 Met Gln Pro Gly Lys Pro Ile Thr Ser Met Asp Ser Ser Pro Val Thr  
 85 90 95  
 Val Ser Leu Pro Asp Cys Gln Gly Ala Leu Tyr Thr Ser Gln Asp Pro  
 100 105 110  
 Val Tyr Ala Gly Thr Gly Tyr Thr Ala Ile Asn Gly Leu Ile Ser Ser  
 115 120 125  
 Glu Pro Gly Asp Asn Tyr Glu His Trp Val Asn Gln Ala Val Val Ala  
 130 135 140  
 Phe Pro Thr Ala Asp Lys Ala Arg Ala Phe Val Gln Thr Ser Ala Asp  
 145 150 155 160  
 Lys Trp Lys Asn Cys Ala Gly Lys Thr Val Thr Val Thr Asn Lys Ala  
 165 170 175  
 Lys Thr Tyr Arg Trp Thr Phe Ala Asp Val Lys Gly Ser Pro Pro Thr  
 180 185 190  
 Ile Thr Val Ile Asp Thr Gln Glu Gly Ala Glu Gly Trp Glu Cys Gln  
 195 200 205  
 Arg Ala Met Ser Val Ala Asn Asn Val Val Val Asp Val Asn Ala Cys  
 210 215 220  
 Gly Tyr Gln Ile Thr Asn Gln Ala Gly Gln Ile Ala Ala Lys Ile Cys  
 225 230 235 240

## (2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

4008484202 205220

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

Asp	Val	Val	Glu	Ala	Ala	Ile	Ala	Arg	Ala	Glu	Ala	Val	Asn	Pro	Ala
1						5						10			15
Leu	Asn	Ala	Leu	Ala	Tyr							20			

(2) INFORMATION FOR SEQ ID NO:286:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

Leu	His	Pro	Ala	Gly	Ala	Thr	Asn	Gly	Ser	Gln	Leu	Ala	Leu	Pro	
1						5						10		15	
Val	Glu	Ala	Pro	Pro	Arg	Ser	Val	Pro	Ser	His	Gly	Glu	Pro	Leu	Gly
	20						25					30			
Ser	Ala	Ala	Pro	Glu	Gly	Leu	Glu	Gly	Glu	Phe	Asp	Asp	Arg	Ile	Asp
	35					40						45			
Glu	Arg	Phe	Pro	Val	Phe	Ser	Ser	Ala	Ser	Leu	Ala	Glu	Ala	Leu	Pro
	50					55						60			
Gly	Pro	Leu	Thr	Pro	Met	Thr	Leu	Asp	Val	Gln	Leu	Ser	Gly	Leu	Arg
	65					70						75			80
Ala	Ala	Gly	Arg	Ala	Met	Gly	Arg	Val	Leu	Ala	Leu	Gly	Gly	Val	Val
	85					90						95			
Ala	Asp	Glu	Trp	Glu	Arg	Arg	Ala	Ile	Ala	Val	Phe	Gly	His	Arg	Pro
	100						105						110		
Tyr	Ile	Gly	Val	Ser	Ala	Asn	Ile	Val	Ala	Ala	Gln	Leu	Pro	Gly	
	115						120						125		
Trp	Asp	Ala	Gln	Ala	Val	Thr	Arg	Arg	Ala	Leu	Gly	Glu	Gln	Pro	Gln
	130						135						140		
Val	Thr	Glu	Leu	Leu	Pro	Phe	Gly	Arg	Pro	Gln	Leu	Ala	Gly	Gly	Pro
	145					150						155			160
Leu	Gly	Ser	Val	Ala	Lys	Val	Val	Val	Thr	Ala	Arg	Ser	Leu		
	165											170			

(2) INFORMATION FOR SEQ ID NO:287:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

Val	Gly	Val	Val	Gly	Val	Gly	Ala	Thr	Ser	Pro	Ala	Gly	Ala	Gly	Ala
1				5				10					15		
Gly	Ala	Gly	Ser	Ala	Gly	Thr	Gly	Ala	Gly	Ala	Gly	Gly	Gly	Ala	Thr
						20			25				30		
Lys	Gly	Arg	Ile	Asp	Ser	Ala	Ser	Ala	Leu	Ala	Ala	Pro	Leu	Ser	Thr
						35			40				45		
Gly	Leu	Leu	Ala	Val	Pro	Ser	His	Thr	Thr	Asn	Gln	Arg			
						50			55			60			

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

Met	Ala	Asn	Thr	Gly	Ser	Leu	Val	Leu	Leu	Arg	His	Gly	Glu	Ser	Asp
1				5				10					15		
Trp	Asn	Ala	Leu	Asn	Leu	Phe	Thr	Gly	Trp	Val	Asp	Val	Gly	Leu	Thr
						20			25				30		
Asp	Lys	Gly	Gln	Ala	Glu	Ala	Val	Arg	Ser	Gly	Glu	Leu	Ile	Ala	Glu
						35			40			45			
His	Asp	Leu	Leu	Pro	Asp	Val	Leu	Tyr	Thr	Ser	Leu	Leu	Arg	Arg	Ala
						50			55			60			
Ile	Thr	Thr	Ala	His	Leu	Ala	Leu	Asp	Ser	Ala	Asp	Arg	Leu	Trp	Ile
						65			70			75			80
Pro	Val	Arg	Arg	Ser	Trp	Arg	Leu	Asn	Glu	Arg	His	Tyr	Gly	Ala	Leu
						85			90			95			
Gln	Gly	Leu	Asp	Lys	Ala	Glu	Thr	Lys	Ala	Arg	Tyr	Gly	Glu	Gln	
						100			105			110			
Phe	Met	Ala	Trp	Arg	Arg	Ser	Tyr	Asp	Thr	Pro	Pro	Pro	Pro	Ile	Glu
						115			120			125			
Arg	Gly	Ser	Gln	Phe											
				130											

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

Pro	Gly	Ser	Phe	Ala	Arg	Thr	Lys	Pro	Pro	Gly	Arg	Thr	Ala	Asp	Ala
1				5					10					15	
Pro	Ile	Arg	Cys	Arg	Asp	Ser	Arg	Gly	Thr	Ala	Gly	His	Arg	Ala	Leu
					20			25					30		
Asp	Glu	Pro	Pro	Pro	Arg	Gly	Ser	Glu	Pro	Ala	Arg	Arg	Arg	Ser	Arg
					35			40					45		
Gly	Val	Arg	Thr	Val	Val	His	Asp	Ser	Leu	Ala	Ala	Arg	Arg	Val	
					50			55					60		

## (2) INFORMATION FOR SEQ ID NO:290:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

Gly	His	Gly	Gly	Gln	Ser	Ala	Ile	Gly	Leu	Gly	Gly	Ala	Gly	Gly	
1				5					10					15	
Asp	Gly	Gly	Gly	Gly	Gly	Ala	Gly	Arg	Gly	Leu	Trp	Gly	Thr	Gly	Gly
								20	25				30		
Ala	Gly	Gly	His	Gly	Gly	Ala	Arg	Arg	Trp	Tyr	Arg	Gly	Pro	Thr	Ala
								35	40				45		
Ala	Arg	Ser	Gly	Arg	His	Gly	Arg	Arg	Gly	Trp	Arg	Arg	Trp	Ala	Asp
					50			55					60		
Arg	Gln	Arg	Arg	Gly	Arg	Arg	Arg								
					65			70							

## (2) INFORMATION FOR SEQ ID NO:291:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

Asp	His	Arg	Arg	Arg	Ser	Leu	Ala	Ser	Leu	Arg	Ser	Ala	Ser	Ser	Pro
1					5				10					15	
Ala	Arg	Ile	Thr	Glu	Val	Arg	Pro	Cys	Thr	Pro	Leu	Leu	Glu	Arg	Ser
								20	25				30		
Ala	Pro	Gln	Ser	Gly	Ser	Arg	Asp	Pro	Phe	Arg	Pro	Trp	Pro	Ala	Asp
								35	40				45		
Ala	Gly	His	Ala	Arg	Ser	Pro	Ala	Trp	Tyr	Arg	Leu	Gly	Ala	Gly	Asn
								50	55				60		

Pro Ile Pro Val Arg Ala Ala His His Glu  
65 70

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

CCGCACGTTAA CACCGTGAAT TGAAGGGAGC CGCTGGTCAT	60
CGAACGTTA TTGACCGGCC GGAGGCCACT CGCGTCAC	120
TTTCACGGCA ACGAACGGCG GACACACAC	174
TTGACATTGCA ACAGCACGGC CGCG	

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

TCGCAAAACGG GGTGACGTTTC CGTCCGGTGG CGCTAGAGAG	60
TTTGTCGCAC TTTCCGGTGA CGCTGGCGCG GCACCGCAGC	120
ACCCGGTGAGC TCACGCTGCT AGTGGAGGTG CTCGACGGTG	180
CGCTGGGCAC GATGGCGGCC GAAAGCCTCG GCAGGGGGGT	240
GCTGGCTGTG TTACAGCGCT TGGTCACGCCG GTGGGATCGG	300
CGCGCTCGCG ACGTCGACAT TCTGCTGGAC GGCAGACCG	360
ATCCGACCGC ACCGGGCGC CGCGATGTGA CGACGTCGGC	404
ACCCGGCGT CAGGTGGCGT CAGTTGGCG GATGGTCAGC	
TCGCGGAAT CGCTGCAGCA CAGCTTGACT CGGTGGCGGT	
GGAGCTGGAT GCATTGGCCG ACCGGCTGGC CACT	

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

Ala Asn Gly Val Thr Phe Arg Pro Val Ala Leu Glu Ser Leu Ser His	
1 5 10 15	
Phe Pro Val Thr Val Ala Ala His Arg Ser Thr Gly Glu Leu Thr Leu	
20 25 30	

Leu Val Glu Val Leu Asp Gly Ala Leu Gly Thr Met Ala Pro Glu Ser  
 35 40 45  
 Leu Gly Arg Arg Val Leu Ala Val Leu Gln Arg Leu Val Ser Arg Trp  
 50 55 60  
 Asp Arg Pro Leu Arg Asp Val Asp Ile Leu Leu Asp Gly Glu His Asp  
 65 70 75 80  
 Pro Thr Ala Pro Gly Leu Pro Asp Val Thr Thr Ser Ala Pro Ala Val  
 85 90 95  
 His Thr Arg Phe Ala Glu Ile Ala Ala Gln Pro Asp Ser Val Ala  
 100 105 110  
 Val Ser Trp Ala Asp Gly Gln Leu Thr Tyr Arg Glu Leu Asp Ala Leu  
 115 120 125  
 Ala Asp Arg Leu Ala Thr  
 130

## (2) INFORMATION FOR SEQ ID NO:295:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

GTCTTCGACGG	CTACGAGTAC	CTGTTCTGGG	TGGGGTTGTC	GGGCGCCTAC	GRCGACAAGG	60
CCAAGAACAC	CACCAAGGCC	GTCGCCGAGC	TGTTTCGCGGT	CGCGGGGGTG	AAATACTTGG	120
TGCTGGCGC	TGGGAAACC	TGCAACGGCG	ACTCGGCGCG	CCGCTCCGGC	AACGAGTTCC	180
TCTTCCAGCA	GCTGGCACCA	CAGGGCGTCA	AGACCCCTGG	CGGTTTGTTC	GAGGGTGTGG	240
AGACCGTGA	GCTCAAGATC	GTTGTCACCT	GCCCGCACTG	CTTCAACACC	ATGGCAAGG	300
AAATATGGCA	GCTGGGGGCC	AAACTAACCC	TGTCGACCA	CACCCAGCTG	CTCAATCGGT	360
TGGTGGCGGA	CAAGAGGTG	GTCCTCTGCA	CTCCGGTTTC	TCAGGACATC	ACCTTACCCAG	420
ACCCGTTGCTA	CCTGGGTTCG	CACACAAAGG	TCTACGAGGC	ACCACGGGAG	CTGATCGGTG	480
CCGCGGGGGC	CACCTGAGCC	GAGATGCCG	GCCATGCCGA	CCCGCAG		526

## (2) INFORMATION FOR SEQ ID NO:296:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

CTCGCCGGCG	TGATCTGGCC	GGCGAACTTC	GTCAGTGCAT	CCAGACCCA	ACGATCATCG	60
ATCAGGGCGA	TGCCCATGAT	CACCGCACCG	GCCACCAAGCA	CCGGGGCAT	GCCGGTGGAA	120
TAGACGAACC	CCCGGGTAGG	TGCCGGAAAGC	TGGGAGGCAA	GAAGAGCGC	GCCGACAATG	180
CCCAAGAACCA	TGCCCCACCC	ACCCATCTGA	GGGGTAGGGC	TGACGTTGCA	ATCTCGCTCC	240
CGCGGGTAGG	CGACGGCTCC	CAGGGCATCT	GCCAGCATCC	GCACCGGACC	GGTCGCAAAA	300
TAGGTGATGA	TCGCGCGCGT	CAGCCCCGACC	AGCGCAAGCT	CACCGCAGCGG	GACACCGGGC	360

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CCCGCGATAGG ACAGGGCGAG CAAGCCACCG GCAACGCCGG CCACATCGCT GGACACCTCG	420
AGACCGTACT GCACCAACCT GAAGAGCTGA CAACTCGCCG AACGTGCAAC AGCTGCGAAC	480
AATTGGG	487

## (2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

ACGAAGCGGG AGAATATGAG CGGGGGCAC CCGGCATGTA CGAGCTTGAG TTCCCGGCGC	60
CTCAGCTGTC GTCGTCGAC GGCGTGGTC CGGTGTTGGT GCACGCTTTG GAAGGTTCT	120
CCGACGCCGG CCATCGGATC CGGGCTGGCG CGGCCACACT CAAGGGGCC CTGGCACACAG	180
AGCTCTTCGGC GTCTTCGGC ATCGATGAC TACTGGACTA CCGCTCGCGG CGGCCATTAA	240
TGACTTCTAA GACCGATCAT TTACCCACT CGCATGATCC TGAGCTAACG CTGTATGCGC	300
TGCGGACAG CATCGCGAC CCATTTCTGC TGCTGGCGG TTGGAGCCG GACCTGAAGT	360
GGGGGGGGT CATCACCGCC GTCCGATTCG TGGCGAGCG CCTGGGTGTA CGGCACAAAC	420
ATCGGCCTGG GCACCGTCCC GATGGCGCTT CGGCACACAC GACCGATCAC GATGACCGCT	480
CATTCCAAAG CGACGGGAGCT ATCTCGGTT TCAACCGTT CGATCTCC	528

## (2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

CCAAGCCCGT CAAGGGACCG GTGCCGCCCT TGCTCCGGT GCGGCCGACG CGGGCGTTGC	60
CGCCGTGTC GCGCTTGCCT CGCGTACCGG GGTTCCTAC GGTGCGCCCG CCCGGCACCA	120
TGGCCCGCT GTTTAGCGG TTTTCGCCGG CCCCGCCGTC ACCGGCTTTG CGCCATCGC	180
CGCCGTGTC GCGCTGGTG CCTGGTTGAC GTATTGTTCC ACCGGCCCGG	240
CCCTTGACCC TTTGGCGGTG TCAGATCCGGG CGTCGATGGA TCCGGCGACC ACGACGTGG	300
AAGCTCTGCC TGCGCCGCCA GCGCCCAAC TGTTGCGGG CTCTCGCAT TTGGCCCCGG	360
CCGACGAGAT GATGGGACCC ACCGGAGCTC CGGGCCGCTCT GGGGGAGGCC AGCGGGGGTT	420
CGCGGTCACT CCATACCGGA CGGTGCCCG CGCGCTGGGA GATTTCGAGG CTGCGTTGCA	480
CCAGATCGAG CAGGGGTGTG CCCAGGGACT GGTTAGGCC GTGGCGCCG CGGTGTTAGC	540
GGCGAGCGCA ATATCGGTGC CCACTCGACC CAACCGCGAC TCCATAAGCG ACACCATTG	600
CGGTGATGC	610

## (2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid

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(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

Phe Asp Gly Tyr Glu Tyr Leu Phe Trp Val Gly Cys Ala Gly Ala Tyr  
 1 5 10 15  
 Asp Asp Lys Ala Lys Lys Thr Thr Lys Ala Val Ala Glu Leu Phe Ala  
 20 25 30  
 Val Ala Gly Val Lys Tyr Leu Val Gly Ala Gly Glu Thr Cys Asn  
 35 40 45  
 Gly Asp Ser Ala Arg Arg Ser Gly Asn Glu Phe Leu Phe Gln Gln Leu  
 50 55 60  
 Ala Gln Gln Ala Val Glu Thr Leu Asp Gly Leu Phe Glu Gly Val Glu  
 65 70 75 80  
 Thr Val Asp Arg Lys Ile Val Val Thr Cys Pro His Cys Phe Asn Thr  
 85 90 95  
 Ile Gly Lys Glu Tyr Arg Gln Leu Gly Ala Asn Tyr Thr Val Leu His  
 100 105 110  
 His Thr Gln Leu Leu Asn Arg Leu Val Arg Asp Lys Arg Leu Val Pro  
 115 120 125  
 Val Thr Pro Val Ser Gln Asp Ile Thr Tyr His Asp Pro Cys Tyr Leu  
 130 135 140  
 Gly Arg His Asn Lys Val Tyr Glu Ala Pro Arg Glu Leu Ile Gly Ala  
 145 150 155 160  
 Ala Gly Ala Thr

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 161 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

Arg Arg Arg Asp Leu Ala Gly Glu Leu Arg Gln Cys Ile Gln Thr Pro  
 1 5 10 15  
 Thr Ile Ile Asp Gln Ala Asp Ala His Asp His Arg Thr Gly His Gln  
 20 25 30  
 His Arg Gly His Ala Gly Gly Ile Asp Glu Pro Pro Gly Glu Cys Arg  
 35 40 45  
 Lys Leu Gly Gly Lys Lys Asp Gly Ala Asp Asn Ala Gln Glu His Arg  
 50 55 60  
 Gln Pro Thr His Pro Arg Gly Arg Arg Asp Val His Ile Ser Leu Pro  
 65 70 75 80  
 Arg Val Gly Asp Gly Ser Gln Ala Thr Gly Gln His Pro His Arg Thr  
 85 90 95  
 Gly Arg Lys Ile Gly Asp Asp Arg Arg Gly Gln Pro Asp Gln Arg Lys

100	105	110
Leu Thr Gln Arg Asp Thr Gly Ala Ala Ile Gly Gln Gly	Glu Gln Ala	
115	120	125
Thr Gly Asn Ala Gly His Ile Ala Gly His Leu Glu Thr Val Leu His		
130	135	140
Gln Pro Glu Glu Leu Asn Thr Arg Arg Thr Cys Asn Ser Cys Glu Gln		
145	150	155
Leu		160

## (2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

Glu Ala Arg Glu Glu Pro Gly Gln Pro Gly Met Tyr Glu Leu Glu			
1	5	10	15
Phe Pro Ala Pro Gln Leu Ser Ser Asp Gly Arg Gly Pro Val Leu			
20	25	30	
Val His Ala Leu Glu Gly Phe Ser Asp Ala Gly His Ala Ile Arg Leu			
35	40	45	
Ala Ala Ala His Leu Lys Ala Ala Leu Asp Thr Glu Leu Val Ala Ser			
50	55	60	
Phe Ala Ile Asp Glu Leu Leu Asp Tyr Arg Ser Arg Arg Pro Leu Met			
65	70	75	80
Thr Phe Lys Thr Asp His Phe Thr His Ser Asp Asp Pro Glu Leu Ser			
85	90	95	
Leu Tyr Ala Leu Arg Asp Ser Ile Gly Thr Pro Phe Leu Leu Ala			
100	105	110	
Gly Leu Glu Pro Asp Leu Lys Trp Glu Arg Phe Ile Thr Ala Val Arg			
115	120	125	
Leu Leu Ala Glu Arg Leu Gly Val Arg Gln Asn His Arg Pro Gly His			
130	135	140	
Arg Pro Asp Gly Arg Ser Ala His Thr Thr Asp His Asp Asp Arg Ser			
145	150	155	160
Phe Gln Gln Pro Gly Ala Ile Ser Asp Phe Gln Pro Phe Asp Leu			
165	170	175	

## (2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

205220-Et848007

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

Lys Pro Val Lys Glu Pro Val Pro Ala Leu Pro Pro Val Pro Pro Thr  
 1 5 10 15  
 Pro Ala Leu Pro Pro Leu Pro Pro Leu Pro Pro Val Pro Gly Phe Pro  
 20 25 30  
 Thr Val Pro Pro Pro Gly Ser Met Ala Pro Leu Phe Arg Pro Phe Ser  
 35 40 45  
 Pro Ala Pro Pro Ser Pro Ala Leu Pro Pro Ser Pro Pro Leu Pro Pro  
 50 55 60  
 Leu Val Gly Val Ala Ala Trp Leu Thr Tyr Cys Ser Thr Gly Pro Ala  
 65 70 75 80  
 Leu Asp Pro Leu Ala Val Ser Ile Ala Ala Ser Met Asp Pro Pro Thr  
 85 90 95  
 Thr Thr Cys Glu Ala Ser Pro Ala Ala Ala Ala Gln Leu Cys Arg  
 100 105 110  
 Gly Ser Cys Asp Leu Ala Pro Ala Asp Glu Met Met Gly Thr Thr Gly  
 115 120 125  
 Ala Cys Gly Arg Leu Gly Glu Ala Ser Ala Gly Ser Arg Ser Arg His  
 130 135 140  
 Thr Arg Arg Cys Ala Ala Ala Ser Glu Ile Cys Arg Leu Arg Cys Thr  
 145 150 155 160  
 Arg Ser Ser Ser Gly Val Pro Arg Asp Trp Val Ser Pro Leu Ala Pro  
 165 170 175  
 Pro Leu

## (2) INFORMATION FOR SEQ ID NO:303:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

AATTGGGCAC	GARCAGCAC	AACACCGGCT	TCTTCAACTC	CGGGCACGTC	AATACCGGTA	60
TCGGCACAC	CGGCAGCTTC	ACACCGGCA	GCTTCAACTC	GGGGGATTC	AACACCGGGG	120
ATTTCAACCC	ANGCAGCTAC	CACACGGGA	CTCGGAAAC	CCGGCGATT	TACACCGGC	180
CCTTCATCTC	CGGCAGCTAC	AGCAACGGGT	CTTGTGGAGT	GGAAATTATC	AGGGCTCAT	240
GGNTGCACCC	GGGCTTRCGA	ATCCCTCGK	CCAAATTCAC	TCCCTCNACAA	GCTTGCGGCC	300
GCACCTSAGC	CCGGGTGAA	GATTGAGTTT	AACCGCTNAN	CAATAACTAG	CATAACCCCT	360
TGGGCCTCT	AAACGGGTCT	TGAAGGGTTT	TTTGTGAAA	GGGANGAACTA	TATCCGGATA	420
ACTGGGCCTAN	TACGAAAAGC	CGCACCGATC	GGCTTCCCAA	CAGTTGGCC	CCKGAAATGGC	480
AATGGACCCN	CCTKTTACCG	GSCATTAAACN	CGGGGGTGTN	GGKGTACCC	CCACGTMNAC	540
GCTACCTTGC	CANNSSCTN	RSGCCGTCTT	TCTTTCTTC	CTTCCTTCTC	CCMCTTGC	600
GGTTCCCTNC	AGCTCTAAAT	CGGGGNCCCC	TTTGGGGTTC	CAATTTATTC	TTACNGSCCC	660
CCACCCCAA	AAATNTATNG	GTTTAATGTC	CTTMTTGGG	CNTCTCCCTA	WTNANNTTCA	720
TCCCCCTTNA	CTTGRSTCC	CTTCYTTATW	NTGAMNCTNT	TTCCACAYGGA	AAAMNCTCCA	780
CCNNTTSSGS	TTCCCTTGA	WTTATMRGR	AATTSCAATY	CCGCYTTKGG	TTMAANTTAA	840
CYTATTTCNA	ATTTCCCCGM	WTTTMMNATR	TTNSNCKCGM	KNCTCCNRKA	SSGNNTTCTCT	900
CCCCCYTSS	GKTYCCCCRN	G				921

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## (2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

AATTGGGCAC	GAGATANGGG	CGCACCGGGG	TCCGCA	GGCGGACCGT	CGCCAGCAC	60
ACCGGGTCA	ACAGCACAC	GGTGGCGTCA	ANGAGAGCG	CCGGCGTGT	GGCGGCCGAG	120
ACGGCRAACA	CCTGGCGTAG	CAGTCGGTGC	GACTCCCGC	TCGCTCGANC	CATGGCGCG	180
CGGGCTGCT	CGAACANGCC	TTTCGTCGTC	ACAGCTTACG	CAGCANCCAA	ACCGCACCCCA	240
GAAANCCACA	CGCCGCCGCG	CGGGANCCAA	TGCGGCATCG	KCTGCTGGGG	CGANATCCCC	300
CGATGGCTA	CANGATGACC	GCTGCCGGA	CGCGCCGCGT	GCCTCCGGGC	AGCCGCGTGG	360
GCSSGGCAAC	CGCGAACCCA	NGAACACCGC	AAGCAGTATC	ANCGCAACAG	CAATTGTCAA	420
GGGCTAAACG	CTTCACATC	AGGGATCTCG	CGCGGCCACAC	CCGTCGGMTC	TGCAAGSGCGA	480
CCCCNTCCCTN	GGGGCGNCAC	TCNTCAAGA	TGCGNATCNA	CAGKCTAGGT	CTTCGGCCGA	540
TATGSAAGGN	CCCAACGNT	TTAAAGCGGC	AAAAAAASTC	TCCCCANTGGA	TAAAATCAGC	600
CGGGGANCC	CCCGTGSCMM	NTGNYCAGK	ATTNTTCAC	MGGTTTNAAGC	CGGGKTGCGN	660
GCCAACTKG	CAAAMTTAAC	NTGNGGNTY	CGGGCGCGTA	ACCGGCNNTK	NGCCCCCTTAA	720
AAAACCGNC	YTTCCTGAT	TAMMACCGG	CCCCCAWTGG	CGGKTGKTC	CANGNTYAAC	780
AMCCYCCCS	MNGGGKTTGS	SAACCTTC	CGNGGGTTC	NTKGTTSCTY	AWMCCCCCCC	840
AAACCSGKYG	GGKTGCRCTN	WASSAMNCCC	CMNGYYCTTT	TAAGGGCAN	KNRAAWGKYT	900
CCTTGGA	AAATTCATYC	GAAYAYYCTC	CTYMMGSSCN	CTTCKWRTTYN	NRNNGGAACCS	960
AMWTNYCCNC	GWTTCAWTG	GGTCGAGSMN	AAACKCTTYY	TTTYCYGSSC	STCCMGGSNC	1020
SGGTKNANAN	AAASATTIMC	YCCNNNANKK	YYCYSSGCTT	CYKMGRRNRR	GMGAACCCGR	1080
GS						1082

## (2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

AATTGGCAGC	AGTGATCGCG	CTGAAGCCGG	TAGCGGGGT	GGCTCGGGTG	GTTCGCAAC	60
RAATTCGCT	CGANGTGGTC	TGGTAGGG	GTGTCANAA	CGTGGCGCGC	GTGCGCGCGG	120
ATCTGATCG	CGCGGCGCTG	GTGCACTG	CGCGGGCGTGT	GCAGTCGGAT	GCAGGAAATG	180
TITGTGTTCT	GGTTGTACCA	GCGGAAGAAC	CGGTCGCGAGT	GCACCCGGGC	CGCCTCGATC	240
GACTCGAAC	GTTCGAGGAA	ATCGGGCGG	TACTTGTGAGT	TCTYGAAC	TGGCTTCAGAC	300
AACGGGTATG	CTTGTGTTG	TGCGGGCGGT	AGTCGGACCT	GGTGACACCG	AAAGTCGGCA	360
NCANCAATGC	CACCGTTTG	GAACATCATC	ACAACCCCCG	TCCCGCTCMA	GGTCACTTGT	420
NCGGCGCTAA	TTTNTYGGGC	GGCAAGGGTT	TGCGCGTCA	KCCGCTGGC	CAAAAATTCG	480
ANTCNCSCTA	AGGCCNCCTA	CCNCCCAAAC	AMGTTACCGG	ANAAAANATY	CAAAGYAC	540
CYTCCGGKTN	TTATANCTYC	CCYTTGSTY	GGGCCCCCN	CYYTGKKNAT	ACCCCTNCCA	600

AWTCCCACN	CCCKCCAANA	RCYKGGGGCC	CCCNCAC	CGGGKGAAKA	WTAATTAAA	660
CCCYACMAW	ACTWWMNACC	CNNGGGSCCY	AAMCGTYNRR	AGGTTTTSCT	NAAAGAAASA	720
ANTCGGAAMC	CGGNTSTACC	AAAASCCCK	CCNWTCCTC	CRASATTGSC	NCCSAWKS	780
AKGCCCCCNY	TCSGCNWNNC	CSGGGKKKT	KKGTTNCCT	WMRCWWMYTS	GGCCNASCCN	840
CKYYSSMYCC	CCCCCTCCCCM	CTCCGNKTC	CCAMCCYANC	MGGCCCCYTM	GKCCCCWKN	900
YKGCCCCCCC	AMMNNNGGGG	WGACCCNTNGG	CCCCMKRRGM	TCCCNANTGA	MCCTCWGNRA	960
MKCYCCNRR	ANMCCSNCC	NGCNCRCKNN				990

## (2) INFORMATION FOR SEQ ID NO:306:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

AATTCCGGTG	GAAACGGGGG	CCTGTTCGGC	AACGGCGCCG	CCGGTGGTGC	CGCTGGGGCT	60
GTTGGTGGCG	CCGGCGGCCG	GGGCCTGTAAC	GCGGGGTGGT	TTGGTCATGG	GGGCCTGGC	120
GGGGTGGGTG	GTGTGANTGTC	GGCCGGGGCC	AACGGTGTCA	CGCCGGTCA	GGATGGGGCG	180
GCTGGTGTG	CCGGGTCCGA	CRACRCTCGT	GCCGCTCGTG	CCG		223

## (2) INFORMATION FOR SEQ ID NO:307:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

AATTCCGGCAC	GANGCGGCAA	CGGTGGCAGC	GGCGGCCACGT	CNGTTGCCAC	CGGGGGGGCC	60
GGGAACGGCG	GTGCGCGCGG	CGCCGGCGGC	GGGGCGGGC	TGATCGGCAA	CGGCGCAAC	120
GGCGGCAGTG	GGCGGAATGGG	CGATGCCCG	GGCGGCCACCG	GCGTCNGGG	CATCRGTGGG	180
CTGTTGTTG	GTGGCGGACRG	CCCAACACGCC	GGGGCGACGA	CCAACCCCT	GCACACCGCG	240
CAGCACRGGC	GTGGCGGCA	GTCAACGGC	CCATCCAGGC	CGTGACCCGG	CGCCCCTGAT	300
CGGCAACGCC	CCAACGGCGC	CCCGGGCAAC	GGGGCCCCCG	GCRGGCACGG	CGGGTGTG	360
TCGGCGCGC	GAAGAACCGG	CGGGTCCGGC	GTCANCRGG	GGGCAGGGCG	AAATGCCG	418

## (2) INFORMATION FOR SEQ ID NO:308:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1049 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

AATTCCGGCAC	GAGGGGACG	ATCGCATACA	CGCCTCGGG	CAGACCCGCC	CGATACAGCA	60
GCTCGGGCAC	CCGGAGCGCA	CAATAACGGG	TCTGGCTTC	CGGCTTGARC	ACCAACCGGT	120
TACCGGGCAC	CAGCGGGGGC	ACCGAGTCGG	ACACCGTAAG	CGTCATGGGG	TAGTTCCACG	180
GGCAGAGATCAC	CCCCCACCAAG	CCCTTCGGTT	GATAGCACAC	CGTGGTCTTG	CCTATCCCCG	240
GCAGCAGCGG	CTGTGCCCTTA	CGGGGCTTC	GCAGGTCCAC	ACAGACTCTGT	GCSTTATAAT	300
TNCGCTTCC	GGGATCAAGAT	CGACAATTTC	CTCTTGCAC	GCCCCATCGGG	CCTTGGCCCG	360
CTCGGCTTGC	AGGAAGTCCA	TGAAGAAC	CGGGGTTCTGC	ATNAACAGGT	CGGGATAGCG	420
GCGGATGACT	GCAGCTCGCT	CGATNACGGG	ACCTTCGCCA	GTCGGTCTGC	GCCGCGCGAN	480
CTTCCGCGCAC	CGCGCTTCG	ACTTCGGGG	NCGTGCAAC	GGAAATCNTAT	CACGGGTTGC	540
CGGTTAAAC	TCTCTTAAT	NCYGGTCAAA	ATTCGGCAAC	TTCTTATCCC	GGCAGGTRCC	600
AACSNANCAA	ACCTCGGCA	GGTTAGGMMT	TCCCCCNCTT	YCAAAAATNC	GGKTTTTGGN	660
CMAATTTCG	CKCNATKGTK	MCMAAGGMMT	CKAANAAKCS	GGGTCTCTM	NTCNGKGAK	720
CCAAMGGKT	TGGGGGAGC	GKNNMCNCAA	CCTWACCTC	KTAANGGNW	TTCCCCCGGG	780
GGGAKKNGA	ATCYCCSNA	NCCCRGGGG	GNMCRARATTC	TYCCGGMCTC	CTCKGGAWTC	840
WGMGTTTCC	AAAAAAASC	CCCAAATTTC	TTTTTCCCR	TRTTGANACW	CTTTTKARCA	900
MMCSAARNS	ANMCNCTCY	CKCTKTKGTT	AAAAGNAYNW	CCCCMAATT	TYTAWTSSC	960
CCSCCGGGGN	CCCNCTNTTT	TSCNMTWCTM	WNYTNCRMCC	MMMSNCKNSG	KKGNRCCNN	1020
CRCCSNCCM	AAWYNTKGYN	KNTATMAGC				1049

## (2) INFORMATION FOR SEQ ID NO:309:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1036 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

AATTCCGGCAC	GAGGGAAATCG	AGAATCCCG	AATGGTGAAG	CCTCGGTGCC	TGCCGTTCAG	60
CCAAGAKTCA	GGGTGAGCGG	CCCCCGGTG	GGAAATGCTGA	SGCCAAACGG	GAAAAGGGTG	120
AGGGCTGGGG	GGATTAATA	GAANNTTACT	GGGATGGAAA	ACCCGGTATT	GATATGTATT	180
GGGGCGATCA	ANGTTGTTGG	AATGGGGGAA	GGCTGAGGGC	GACCTGTTGG	ATTGGGGAA	240
TTGTYRTGGA	CRACAKWG	CAGCGMCGT	GATGGTTTGG	TTSAANTTTT	GTGCCGSCCA	300
CANGGTGATG	GGATGATTG	TGATGGGGCC	SATCGAAATA	TTGGGTATGC	CNACGCSAA	360
CGAGATGYCC	GGGAGCTTCA	TGGCGGGGAC	AACCMASGGT	CCSANGTAAK	GGTTTCTTN	420
ATNTTGTATCG	GGATTCCCGA	ACTMTSTCGA	TGSGCTCSAY	MTSATSGCCC	NACNCWC CG	480
YTATTTTCS	GCCTNAYGGG	ATBAMRGGA	CAA YNTCCCT	CCCMGAAAAC	ACCAACMSG	540
CTCTGGTNSVC	CNC CCRCCNC	AKAACCCRTT	KCTGTRSTMC	CCSMAAATNA	CSCCCSCTTS	600
NACTCCNCSG	AANTNSCCC	CCCSCKNNIT	ATSTYCCCGK	GTTCCCCCMC	CCCTTNAAMC	660
TCCCCGGTT	ACCCCCWNT	SNCNCCCCS	YTAARKMNCR	GCTTSTTNTC	CCCCCYTRMK	720
CNC CCCCCTCK	SACWNCNC	CTCKAACNAC	CCCKCYKGS	TNCCCAATNT	WCMWCKCCNS	780
KTNTNTMCTCK	SCAAATNCR	CCNCRCTCCC	CKKSTSTC	WTATAAAACC	WCWYAWYNN	840
KCNCWMAWTA	MGACWCTCN	NCCCCCNCK	NTTCTAMWC	CKMCCCKCSW	TWCYCKCS	900
CCMTCTMNA	CYCCCCKTY	NKWMCCCTTC	CCCCCTCCC	MCNMBMKTCT	YCSGKTCWC	960
NCYNTMTCN	CYANANMCKCK	KTCTCTTCCN	CRNTCTCCCC	CCWCCCCCCC	KKCTCTSKCC	1020
CNCNCTCCSC	MMKGSC					1036

## (2) INFORMATION FOR SEQ ID NO:310:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1036 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

AATTCCGGCAC	GAGATCATGTA	ATAGCGGGCT	GGTCAGCACCA	GAAGTGGTCG	GGCATCTCGC	60
GAGCAAGCT	CGTCTGCTCG	CCACAGCGA	GGTCGGCATG	GATGCGGACA	CCTGCGATGT	120
CTTGGATGGT	GTCAGTGTG	AGGTAAAGCC	GGACGGCGAG	CTTTGCTAGC	AGGGTGTCTT	180
GGCTCTTCGG	ACGTGAGGTA	ACCAATAACT	CCGACGCGAGA	CCAACTCCGG	CCCTCGATCC	240
GGGTACCAAGG	CTCCAGCGGT	GCCAGCGCTT	GTGCCCCCTG	GGCCGAAGGT	CAGCTGCTGT	300
GGCATCGGAAG	TTAAAGAACCC	CCGCCATGCC	GTGCGGAAGT	ACGACTGACCC	GAGCAACGCA	360
ACGATCGTGT	TCCCTTCCGT	GGGGGTAAATC	GANCCAGCA	ACCGCACGAG	CCACCAATCA	420
TTGGGATTCG	GCCACTGACC	GACCAACCGC	CTGTGCGACA	CCCAGCGGA	ATTGGTGGTC	480
TTCCCGGGGG	CCGCAACGG	AATCACGSSG	ACCGCGTCGC	CGAASCANCC	GCATANCNT	540
ACATANCAAC	GGNNCTCTGG	CCCACACATTTC	GGGTTTMTGC	CCCTCNGCAA	CSNSAAYNCC	600
CCCAATTCTCG	AACNAAA	TTGGYCCAT	ARNGTYCTCC	CCAAAACACN	AWTCCCCKTA	660
TCCCCGGGGG	GGGGCCCCY	NMNAAAACGG	CCWWAANCC	CCSGGGCS	CGGGTTRWTN	720
CCCCCTGTGCG	GCCCNCCSGG	TTGGTGTGCM	GGSMNTINWN	GGGNTGCS	CCCNNA	780
AAAAAYCKNG	NMNAATYAAA	CCCKYCMAAA	ASKTGGSSC	CCCMARCCGG	GGKAAKKNWA	840
ANTTAACNN	KA	ANNNMCCAAA	NGGGNCTTA	GGKYTTAGGG	TTTSTTNANG	900
ARAAAATMTC	CANATMNSKK	TTNNNAAAA	ASCCSWAKCC	CCCNNNKKNN	CCAANKAARR	960
SRCCCTGGG	TNWNSGGGG	KKKKKTNCMS	KMNNMWTWGR	CCCNCCGCC	NNITWCCTTN	1020
TCCNYGNGC	RNCAGN					1036

(2) INFORMATION FOR SEQ ID NO:311:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1060 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

AATTCCGGCAC	GAGTCGATTC	GATCGAACAC	GCCCGCACCT	GGCCAGGCCA	CATGGCGCG	60
GCCATGGCCA	ACGCCCTACTC	GGCCAACCCG	AATCCATTG	GGCTCTCACC	GCACCCCCG	120
AAACCGGGGA	CGCGCGCATG	GATCAACCCG	CCCAACCCAG	ATCCGAAATA	GGCTCCACAT	180
AATGAGACAC	TGGCGCAAAG	AGCTTGACAG	GGCGCGCACC	ACGCAAGCTG	TTAGACGTGT	240
CGGTTCTGCA	AGAACGGGGT	TGGGCCACCA	AGATCACGCC	GCCCAAGGGC	ATCGAGTCAA	300
CGTTGGGGTG	GTATCGCGT	AACGTCGGCG	CCGCCAAAGAA	ATGACGTTGC	GCATTACCAT	360
GGCCCTGCTG	ATCACCTTG	GCCACCTGCG	CACCANAACT	ATGANCAGCC	TTATGCGGAG	420
TCTCGTGGAC	ATCGCGACCG	GCTCTTAAAG	CTCTTGTGCG	ACATGCTAT	TGCTGANC	480
CGGAATTCTT	NTRCTTGGCA	SAACACTNCA	TGTTNCSSGT	NAACAACCTY	GGTTNGAAA	540
ACANCCAATA	TTGAATTC	ANTCGGGCAM	GAACCGNTTM	CGGAAGKGTGK	TGGGAACGAA	600
TGKTCGCCAA	AAATCTCCGGG	NGGTRAAAW	CCCNNSNATGG	MSAATTTSC	CTNGAACAM	660
AAAAGGTCCTA	AGKYCAAAGG	NGCCCCCCCC	SGNAACCTGG	TGAACCSAKA	WYANRTTCCC	720
WWNTNCAAT	MTTNGGGTCC	KNNTCCCCWT	AAANGGGSNC	CCCNCCRGG	GMGTYTCCCC	780
NNNMGGGMGN	CYCGSCCCCC	AAAAAAMM	MTTCTSGKGG	SMGKKCCCC	CCSGGTWGG	840
GKYYTTAAC	CCGGKGGGT	AAAAAANAN	ACCCCCCAMS	NGGGGGAAA	ATTGNAAWT	900

AAGGKKKTKC SCMACCCCCA AAANMMNNCN AWNCCCGMKG SARGGGGRNY TTMKAGGGMG	960
GNYCCCCCW YCGGGGGNA NAAYAAAAGK NGSNGRGAAT NTTNTTTGK RSSSRNKTTC	1020
TYNTCTYCN CCNMGNRWKG SRAMNTGKTS NSSGGGSGGC	1060

## (2) INFORMATION FOR SEQ ID NO:312:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

AATTCCGGCAC GAGCTTCACC AAAGAGCTGA CATGCCGGT GATGCGACAT CGCATCGAGG	60
GCAATACGGG ATCGGATGNN CCGAANGAN TCTGGCTTC GCTCAACTGG ATTACGGTTC	120
CCAAGGTGAA ACCGTTTGGG CGCAAAGATG CGACGCTTAA CTTGGCTTC CACCGTCAA	180
TGTTNGTATG GATGCTGGAA CCCGCGTGCAG NATAAAGA TTCCGCTGGTC GCGGGGCAACN	240
ATGGATGTCG CKSPTTTCNC CKCGCGTTA AATTGCGSTG GCATGATCTG GCAGGCTATG	300
TTCCGCTAC RCTGCACCCN ATCATGGATC TCGCGCTAAC GAANAAAGTTA TGACATGGG	360
CAAGCGAMTC GGGCATSCNC CGCGCCTATT CGCAACCTGC TGTGTTNTGAA GCGTMTCAAC	420
CGAATGCGC NGGYAAAAGC NGGCTTGGC TGAATTMMAC CNAACCCNTN CNATYCTTTG	480
CCGNGNNNTG CGTCTCTCC AACTCGGKKG SYTGCNCNG TGAAACCCMA CTNCCCCCCC	540
GTTGGGATAA MRTNTTCAAA AACMGGMNNA ACCSGAATNN SAACCTNCCR TCAAANTAMM	600
SAATCAGGGG TTGGGNRCCN CCCNGAAYW TTGCKNCNGGG GMNNTYCTCN GGTTTYNGGC	660
SAAACNTTGC CCRTCYMNNTT TTACAMGGC NCMTNMNTGM GGGSCSNNAS GWCCCCGGKK	720
TNTTTCAAW TCNCNSKTTT TTGGGGGGGG GGYGRTTRMC NCGGGCCCCC GGCCCKKMAA	780
AAAAAMCMAA RRCCNCYGGG KKCCCSNCCM NNATNGGGC YKCRRAACAA ACCCCAAANRA	840
TNGNGMGGGT SMACCSGNNG GYNAAAKGGT TNSCTTMAN MKGMANNCT SGMSCCMNSN	900
NCTKMGGGKTA TTGKGNNGARN AANAMRMMGM RCGGNCGCNM GAAAGGGSMS GSCKSCNNNG	960
NGASNGWGN CRNNGANRCC NCNGYGNMNR NNNGNNNGNNN GGKRNNAACN NMKMCAWSMC	1020
NSNMGGNNNS CGYMTNKGCG	1040

## (2) INFORMATION FOR SEQ ID NO:313:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

AATTCCGGCAC GAGACAANGG CGTGAATGG GATCCGGCG AGCTGGGGGC CGTCGTCAGC	60
GACCTGTTGG CCAAGTCGGC GCGCCGGTT CCGGCTATG GGGCCTAGTT ATCTGCGCCG	120
AGCCTGAACCT CAGGGGAGGA TTTCTGGCGT TTCTCGGCC CCGGCTTCAGG TTCCGGCGAAG	180
TKGGGAACCG TCAGGGTTCG CAAACCCAGCA TCGGGATCGT CGCGTGGTC CAGGACTGGT	240
ANTCTGTATA CTKGGTACA TCGTGGACAA CTGTGGNCAA TATTGCGCGC GCTCCTCGTC	300
NGTCGCGTCC CGCGCGTAA GGTCCANCAC TTCCCTTTTC TCCTGCGC	348

## (2) INFORMATION FOR SEQ ID NO:314:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

AATTCCGGAC	GAGAGACCGG	GTCGTTGACC	AAACGGACGCT	TGGGCGCGGG	CCCCTTGCGT	60
GGCATCAGCC	CTTCTCCTTC	TTAGCAGCCGT	AAACGGCTGCG	TGCCCTGTTTG	CGGTTCTTGA	120
CACCCCTGGT	ATTCAGCGAA	CCGGGGATGA	TCTTGTAGCG	CACACCCAGGC	AGGTCCCTTCA	180
CCCGGGCGCG	GCGCACCCAGC	ACCATCGAGT	GCTCTCGACG	TTGGTGCGCC	TGCGCGGGAA	240
TGTACGCCTG	GACCTCGAAC	TGACTCGTCA	CTTCACCGGG	GAACACCTTCA	GAAGCGCCGA	300
GTTCGGCTTC	TTCCGGAGTGG	TGGCTCGTGC	CG			332

(2) INFORMATION FOR SEQ ID NO:315:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 962 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

AATTCCGGAC	RAGTCGGTCT	AGACGGATTC	AATGCTCCCG	CGAGCACCTC	GCCACTGAC	60
ACCCCTGAGC	AAAATGTTCT	CAATGTTGTTG	AAACGAGCCCT	TCCAGACGCT	CACCGGCCG	120
CGCGCTGATCG	GCAACCGGGC	CAACCGGACT	CCTGGAAACCG	GGGCTGACGC	GGGGCGGGCG	180
GGTGGCTGTT	CGGCAACGGC	GGCACACGGCG	GGTCGGGGGC	GAACGGAACCC	AAAGGGGGGG	240
ACGTCGGGAC	GGCGCCGGCG	GGATTTCTTC	ACCGCGGGGC	CCGGCGGGGG	CCGGCGGGCGT	300
CGCACAAACGG	CACCGGGCGG	GACGNGGGC	CGTNGGGCG	GCTTCTKGAT	GGGCTCCGGC	360
GGTNACGGG	CACGGCGGGC	CCCGGCTCAC	CGCNGTTGG	GACCGGGGGA	CGCGTNACCC	420
CGATCTTCTT	CGCGNCCCG	GAACGGCGG	GGCGGGCCCC	ACATTAKACC	CGCGCGGNACC	480
GGGGMCCCGG	CGGAACGGNG	GGYNTTTTCC	AAACGGCGGGC	CCCGGGAAACCC	GNMGGSTGTT	540
CCTTNGGSGA	AGGNCCAATK	CCCGKCTANC	YYAATCCCCG	ANGGKTGAMC	CTSATGSNCA	600
MYTTMAGGAA	CYTNCCCANT	KTTSGRACCW	CRCCNGGAAA	ASRAWNKNGT	KGGCAAACNA	660
NNTTNCYTTKNA	NATTKGNNNA	AAAANCCCTY	CCWCSGRACT	NCCCCCNNGN	GRGMCNNTNN	720
NTTTYGNCNN	CCCGGSNAAM	RNTTKATTTC	NGGGGGNTCN	GGGTKMNNA	AACCCAAAM	780
MNRRNNKCSA	ANGGGKSNGC	NKNNNMNSGT	TTTYCKNMR	MRNWTRYKNKN	NTCNGARSRN	840
NAAMCNNSNK	NGKKKNNKAA	ARNNNTWTKT	KNSCNCNNCN	GRRNGVRGGC	CKMKGSNMG	900
MCWHNAWRNG	NNGNSCNCKC	NNKMNAAAAA	AASGVNCKS	NSMKNKKKG	NRGGGGGGGG	960
GG						962

(2) INFORMATION FOR SEQ ID NO:316:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

AATTCCGGCAC	RAGAAGACGC	CCGAANGTTT	GCGCTGGCTC	TACAACCTICA	TCAARGCGCA	60
GGGGAAACGC	AACTTCGGCA	AGATCTAGT	TCGCTTCCCC	GAAGCGGTCT	CGATGGGCCA	120
GTACCTCGGC	GCACCGCAGC	GCGAGCTGAC	CCAGGATCCG	GCCGCGAAAC	GGCTTGCCTT	180
GCAGAAGATG	TGTTTGCAGG	TGGCTGGAG	GATTTGCAC	GCGACGCCNG	TGACCCGCGAC	240
GGGTTTKGTG	TCCGCACTGC	TGCTCACCAAC	CCGCGGGCACC	GCGTTGACCT	CGACCAGCTG	300
CACCACTCGT	GCCGCTCGTG	CCG				323

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1034 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

AATTCCGAGT	GTGTGTGGCG	GCGTCCAGAA	GAAGATGATC	GCGAACATCG	CCAGCGCCGG	60
CCAGGCTATG	GTGCGGGTGA	TGGCCGACCA	GCCGATCATC	ACCGGCATAC	AGCCGGCCGC	120
CCACCCCCAC	ACCACTTTC	GTCAGTGGG	TGGCTTGAGC	CAAAGCTGTG	AGACRAACAC	180
ATAAAAACGG	ACCGTGAACCA	GGGCCAGAC	CCCCCGGACG	AGGTTCTGGG	CGCACCATAG	240
CCAGAAGAAC	GAGATCACCG	TCAACGTAC	CCGAGTGCAC	ACGGCTTTCG	GGTCGGCACCC	300
GCTTCGGGCG	CCAAGGGCCG	GCGCCGGTT	CGCTTCATCA	CCTTGTGAT	ATCGGGCTGC	360
GCNACCAATTG	GAGCGTGTG	GGGCCGGCG	CSGCCATCAT	CCCCCCGACN	ANCGTGTGTA	420
GCATGANCAG	GGCGATGAATG	GGGCCGGCG	TCTGCGCGT	CCTGCGGAAT	TCAACTCCGT	480
CNACAACTTC	CGGATGATG	TGAAATGAWTG	AATTAAACC	GSTSAAACANT		540
AACACTATAA	CCCTTGGGGG	CTCTTAAACCG	GTYYTGAANG	GGTTTTTTGC	TTAAAGGAAG	600
AACYATTCC	GGATANCATGG	CSTTNTWARC	GAAAAGGCC	CRCCCATNGC	CCTCCACAGT	660
TTSCCCCTGA	ATGGSAAATG	MNCNCYCKNR	CNNGGNCCTT	AACRCSSGGG	GGNTTTTGTGT	720
MCCNNNCTKA	CNTTMMTGC	ARNNCNGGCC	SKCCCCCTCK	TNTYCCCTCC	NTCCCCCNST	780
TNCNGKTCCC	CNNAMNTNW	ACGGGGGCC	YTNGGGKCRM	TWTKTTTGG	GCCCMCCCC	840
MAANANASAN	GGGGKRNGY	CSTTGGCC	CCACAAARGG	NYCCCCCCAM	YTNRKMCNSY	900
CNNTINKGGNN	CTGTNCKNCG	GAARAMAMCC	KCCCCGNSTS	STTNGTYWAG	GNRWKGNSRG	960
CCSCCCCGGY	MNNNAAYAWN	WMNATNCNS	STNANMAKKN	NNNNNNNSCN	WNGNGNNTCN	1020
SCNSNGGKBC	CSCC					1034

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

ATTCGGCAC GAGCCCACAT'CCGGGCCGC	TCGTTGCATG ACTCGTTCGT	CATCGTCGAC	60
RAGGCACAGT CGTGGAGCG CAATGTTG	CTGACCGTGC TGTCGGTT	GGGGACCGGT	120
TCCCCGGTGG TGTTGACCA CGACATCGCC	CAGCCGCACA ACCTCGGGT	CGGCCGCCAC	180
GACGGGTGCG CGCGGTGATC GAGAAAGCTCA	AAAGTCATCC GTTGTTCGCC	CACATCACCT	240
TGCTGCGCAG TGAGCGCTCG CCGATCGCCG	CGCTGGTCAC GAGATGCTCG	ANGAGATCAC	300
CGGGCCGCCG TGAGTCCGCC TCCCGCAGC A			331

## (2) INFORMATION FOR SEQ ID NO:319:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

ATTCGGCAC GAGATCGTCA CCCTGGCGAC CAGTGCACCC AGGCCACGCC ACCAGTTACG	60
GCTGATGGC CAGAAAGATGG ACCAGGTGGT GCCCATCCCG CCCACCGCAC TGCGACTGAG	120
CACCGGGATC CGGGTCTCA GCTACCGCA TRAGCTGGT TTCCGCATCA CCGCTGACTA	180
TGACGGCCCG TCCGAAATGC AGCACGTTG CAACCGTGTG GAACCTGGGTG TGGGGCGCTCT	240
GGTGGCGCTC ANCGAACATT CCGTGTGTTG GTTTACAAGG ATCGGCSTAA GCGTTCATCC	300
CGCGCACTCC CCANCGCCCG CGGGCGGGGG CGGCCCTCTG TGCCGACCGC CCGAGCGCGT	360
CACTGACGCC ATCTCGTCC CGCTAACCTT CGTGGAGAAGG TGGGTGTGTC GCAAGTTGGG	420
CCCGGTCAAC ATCNATCCGC CGCCGCATGA CGCGTGTGTC TTCCACACCA CNTNSGACNC	480
CCCCCAGGAA CTGGTCCGGC AMTNCAGGAA NTYCGTGTGG GCACCNCTT CTTCCGKTRT	540
GGCYTAACAT CTCNATATCT CGSGCGTTCT CTGGCGTTNC GNCCGGGGCG NCCTTNCNA	600
ATCGGSMMAA ATCCCNACM AAACCCCCCG GGTCTTGSGG GCSGGGNNGC GGCCNAWNCC	660
AAACCCCCCC NTIAAAANTCT TTGKTNCNN CNCSGGCNCC NCNAANS CAN CCCCCTTKGGC	720
NCTTCCCCCC CCCAWTTAA CGCAKGCGSC AAACCCAAAGY TMMGKCCYCY KNAAAAAAA	780
AATTGCSGCCC CCCAANTAA ATTCCCNNGG CCYTTGGGGG CGRANCNYNT TTTMCCSNSS	840
TKGNNAAMC NGGANCCSGG KAAYTMMTKG NAAYCGCCSN AAMBNTTTTC TAANNCCCN	900
YNCCCSGAAA ATTNNAMAAM CMNNKTSNSG GGGGKTTNSC SGKKGRAGGM AAAAANRNSN	960
SKTNMCNNN SANMNCNSNN SGGNSNNNNN NNNCNGYKC CSNAANMCCC CGCGGGGGGG	1020
CCMCCC	1026

## (2) INFORMATION FOR SEQ ID NO:320:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

ATTCGGCAC GAGAAAGACGC CGGARNGTST GCGCTGGCTC TACAACCTCA TCAARGCGCA	60
NGGGGAACGC AACTTCGGCA AGATCTACGT TCGCTTCCCCA GAAGCGGTCT CGATCGCGCA	120
GTACCTCGGC GCACCGCAGC CGAGCTGAC GCAGGATCCG GCGCGAAAC GGCTTGCCTT	180
GCAGAAAGATG TCCTTGAGG TGCCCTGAGA GATTTGCGAN GCGACCCNGN TNACCGGAC	240
GGGTTTGTG TCCGCACTGC TGTCACCAAC CGCGSGCACC CGCTTGACGC TCGACCAGCT	300

GCACCACTCG TGCCGCTCGT GCCG

324

## (2) INFORMATION FOR SEQ ID NO:321:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

ATTCGGCAC	GANGCGTGCC	GCTNAACACC	AGCCCGCGGC	TGCCAGATAT	CCGGACTCG	60
GTAGTGGCGC	CGGTGGCGTC	GTGGCTCTCC	TGACGGGGCG	CGGGGACCAT	AAGGTCGCTM	120
ATGCCCAAGGT	AGCGGCCCCAG	GTGCGATGGAG	TGCGATGATG	TGCGACTCTC	CAGCTCGCCG	180
ACCGGGAGCT	TGGCATCGGG	CCTGATCAGC	CAGGACGCGT	AGGACAAAGTC	GATCGAATGC	240
ATATGTTGCC	CCAGAGTGGC	CCTGCGAMTTC	CNGCGTGCCTC	CACGGCAAAAT	GCCTTGATT	300
CTACTCGCG	TANTGTTCCC	CGCGCCTG	CGGGATGAAT	GGGAACCGCA	SGATGGCGAC	360
GAACGGGTCT	GANCTCAGGT	TTGGCGCTT	GGCGCACAGTG	GTCNACANCC	GGTACTCGGC	420
ATANATCTGG	CCCNAAATCG	GGCGCGACGG	GGCCACACNAT	AANAACGGGC	ACNACAAATCG	480
CCGGCCCGGT	TCACCCNAACA	ACANCTTGSC	ATCGGATTTT	GTCcccancg	CTCAANCCGT	540
CCCGAACGCC	TCTNCCGGCG	NACTTTTCTT	NNAWTAACTG	CCGCTTCCGG	CCCTGGNGCA	600
WTAAATGGGA	AACCCTNCC	CCACCTTGAA	GGGGTTGTTG	NATTTTTACT	GSTAACCCCCG	660
AATTNTTCCG	GANTCGTCN	KCCGGGTTT	YSTNTTCCCC	ACCTTINGNAN	GGGCCGGCCA	720
AGSTTTTCTT	SYTGAAGGGG	GAACCAACCA	TTTNTTYTNN	AACCSMNAA	MYMTTYCSG	780
MNAASCCNKT	CCCCTTAAC	CAMGGSGTNN	AACCGKTMNG	NGKGTAaaaa	GGGSKNNKTG	840
NCCCCYMM	GGGGRAAAA	TSTKTCNNCG	GGGGCKAAAW	ACCCMMMYGN	GTGKKKNKSS	900
GCSAAATT	NMMRACTKN	GGGGCGSSGA	NNTTTNAAG	MSCCCCSNN	GSTGKCCCN	960
NTTTCNNAA	WMKKGKWNM	SNMNSCSNNG	GKYNSGGSNN	NNAAGMGGGG		1010

## (2) INFORMATION FOR SEQ ID NO:322:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

ATTCGGCAC	GANGCGTGCC	GCTNAACACC	AGCCCGCGGC	TGCCAGATAT	CCGGACTCG	60
GTAGTGGCGC	CGGTGGCGTC	GTGGCTCTCC	TGACGGGGCG	CGGGGACCAT	AAGGTCGCTM	120
ATGCCCAAGGT	AGCGGCCCCAG	GTGCGATGGAG	TGCGATGATG	TGCGACTCTC	CAGCTCGCCG	180
ACCGGGAGCT	TGGCATCGGG	CCTGATCAGC	CAGGACGCGT	AGGACAAAGTC	GATCGAATGC	240
ATATGTTGCC	CCAGAGTGGC	CCTGCGAMTTC	CNGCGTGCCTC	CACGGCAAAAT	GCCTTGATT	300
CTACTCGCG	TANTGTTCCC	CGCGCCTG	CGGGATGAAT	GGGAACCGCA	SGATGGCGAC	360
GAACGGGTCT	GANCTCAGGT	TTGGCGCTT	GGCGCACAGTG	GTCNACANCC	GGTACTCGGC	420
ATANATCTGG	CCCNAAATCG	GGCGCGACGG	GGCCACACNAT	AANAACGGGC	ACNACAAATCG	480
CCGGCCCGGT	TCACCCNAACA	ACANCTTGSC	ATCGGATTTT	GTCcccancg	CTCAANCCGT	540
CCCGAACGCC	TCTNCCGGCG	NACTTTTCTT	NNAWTAACTG	CCGCTTCCGG	CCCTGGNGCA	600
WTAAATGGGA	AACCCTNCC	CCACCTTGAA	GGGGTTGTTG	NATTTTTACT	GSTAACCCCCG	660

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AATTNTTCG GANTCGGTCTN KCCGGGTTT YSTNTTCCCC ACCTTNGNAN GGGCCGGCCA 720  
 AGSTTTCTT SYTGAAGGGG GAAACCCAAAC TTTNTTYTYY ACCSCMNAA MYMTTTCG 780  
 MNAASCNNKT CCCCTTAAC CAMGGSGTIN AACCGKTMNG NGKTAaaaaa GGGSKNNKTG 840  
 NCCCCYMAN GGGGRRAAAAT TSTKTCNNCG GGGCCKAAAW ACCMMMMYGN GTGKKKNKSS 900  
 GCSAAATTNTT NMNMRAACTNN GGGGCSSGA NNNTTNAAAAG MSCCCCSNN GSTGKCCNN 960  
 NTNTCCNNAA WMKKGNWNM SNMNSCSNNG GKYNSSGSNN NNAAGMGGGG 1010

## (2) INFORMATION FOR SEQ ID NO:323:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

NGNGGGGWN SNTCAYCAYCA YCACSGGGYW CWATTGCGGC CGCAWCTTGT MAASAGATCT 60  
 CGAAYTCGGC AMGAGGGAMT CKTCTMCNNCC GCTGTGCAAN CCAATRAGGC CTRATAATTY 120  
 CCACCTTACA AAAAACCGTT GTGTGAYTT SCGGRRAATR AAGGGCCGG TNTCAACWYC 180  
 GCGCGGTCTT CCRATYCCG TKTGTAMCT GCKGGGTTSR AAAYCCCGG TGTTGGAYCC 240  
 CCGGATTGAA ACTGGCGGTG TGAACATGCCG GKTGTTSGCSA TCCGGKWWAT GAMSTCRGG 300  
 ATTAAAAAAC CGGKKTGGN GCTGSNCGTG CCAAATNCGR AYCCRATAYC CCATGGCTTG 360  
 KYCTYCTCCK CCGGKKTGAA AAYCTGGGT TCTCTATACTG YGCCCTAAAK GCAAWYCKGG 420  
 GCTGYCMMTK TTGCKGSSGT CCNAATTATC CACCASCGGT TCTCTTCATTA CCNAACNCG 480  
 CKTGGCWCC AGMCCGRAAA AAAAKAATAAT RAKAAKGGT CATNYCCAA ACCNCGGCCN 540  
 CCCNANTCN CTCGNTNCC MSCNCNCCTA GCGGTNAAGK TKGSSAAAYTT CTMMAACCCC 600  
 CAAANCCCCA TAACNTNCGA GAASAAACCC CTYCNCGGGY GVCNWNCAAA ACASCTNTAT 660  
 TTGCTKSTTT CGGGMWCCGT GCGGCCNAAA YCCCAAATA STTTYTGGGT CONAGAKAAA 720  
 ACCNCNGGCN CCMCCCSNNA NWATYTCTT KGGCAANCC CSAAACCTTR TCMNACCNCK 780  
 ATRMTCCTT CCCCVCSTAAT TGGYCGGRAT NGCSNCCTY TCCTAAKKSC CAKWNWNNGN 840  
 GRRNNACCMIA ACCCCAAGTY CCMNAAATN GKCCCCGCTC CNAACACGNK TYYTCCSAAA 900  
 ASCCCCCCCCC CCCCCCCCCRAA ACACCCCNKA RKANTNCCCA AACANCYNGK GGCCCCCCCC 960  
 CAAACMAAAAM AMCCCCCSGM RMACSGGGNN NMCCCCGGKK KTTTTCTTT TKCCMRSCCC 1020  
 AAMGCAMWSY KSKTNMAAA GGAAGRANCN TYCCSANANM TCCCNWRSW CCGSGWMGN 1080  
 GAASMCCCC CS 1092

## (2) INFORMATION FOR SEQ ID NO:324:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

GGGGGGNNN NATACATCTT CYGTYACGG GGGMTCTAKT GGGGGGCCG AATCTNGTA 60  
 ASAGATCTCT NAMTCGGC ACACCCACTW GACAACTASYT CGNGCNMTCC GTGTCCTNKA 120  
 TCGCAAAACG NGTRACASAC ASACACRTA GTGTGCCCCAC CASCAAYTCK TTGGGACTC 180  
 GCTRACCGGY TGCCCCNACG CCACGTYGCS CWTCTATCCC RACGCCGGCC ACGGGYGGGG 240

ATATTCAGG	CACCAACGCC	AGTTTGGTGG	ACAATGCCCT	GGCAKTTTC	TCRAANTTCG	300
TGAAACCGAA	TTCNSTMGTG	ACCNCCAARG	CCCCSNCCNR	AACARTTGGG	WTCCGGTGT	360
CTCCCCACCG	KTTTCCGGGG	GTNTCCGGCAN	AANCACCCC	WTGGWTTCTM	TNCNCGCACC	420
GGGGCGACAA	NTCGGGTTGC	AATTTCGCA	AYCGGGGGCG	GGATTCSCCA	AACGGGTGCG	480
GAAACTGTTY	YCRAGAMCCG	GGAKCCGCAA	TTTCGGGCR	ANAAATTTCN	YCNACCAACT	540
GCTTRTACTT	CCCGGACCGT	AACMANTTC	ATCGTCNTNN	CCTCTGCCT	TGGGGCAGGG	600
CKAAAYACCC	CTMTKGTTT	CGCAACCTGC	GGGCCAACCT	CCNAMCCRCA	CTTTCNATT	660
GGNTCGAATT	SCCCCCGGT	RANAACSSCC	NTGGCCNNYT	CGGASSAAA	NGGGCCCTNT	720
KGGCNSSCCC	AGTAANACCC	TACCNNAUTS	CAWTCTTGC	CAAASSTKGG	ACGAANSKTG	780
GGNTTCCGGK	ATTTYGTTS	GGNCNCCCTN	TATNGSNTN	GGGCKCYNC	NCSTKIGKCA	840
NASSKAYCCS	NGNKGGGGGT	ACCCCTCIMG	GGGGTTTTT	NSSGCCCCC	AWAYGNKSTG	900
GCCCCNNGG	GGAAKAATWT	MWWTMCNSGG	GGGAATTTT	NTSTGGAMCS	SGGACYCCCR	960
GGGGGKTTTT	TCCCCNCNSA	NNAWANGGG	GGGGGAAANAYT	NTGNSGNGGG	KWNNTTATT	1020
YTYYCYCTTM	TKACMSGGG	GTTCKKAKNG	GGGGGAGAAA	ANAAAAAAA	RAKGYKNTT	1080
TSKNCACNCT	GKWNWNWANR	NAGAGKTCCT	CKCKCCNCSG	SNTTTCTTT	MGNGSYGGG	1140
GNNNNNNAAA	ACNKSRRMAC	KCSYTYCCCG	CGYCTCCTCC	NCNGGGYGS	NGSCGNSTYN	1200
GNNKGRKWT	TNTMGNGTN	SCCTCCNCCC	GCKKNNTGTC	TMTCNMYGSG	C	1251

## (2) INFORMATION FOR SEQ ID NO:325:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1099 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

AYATCGGCAC	MGAGTATCAC	CAAKCTGYGT	GGCCCAGCAA	AGTGGAGGCTA	TTACTACCTG	60
TATGTGATCC	TCRACACTY	CTCCCCCTAC	KTGGTCGGGT	GGATGTTGGC	CTCGCKTGAK	120
TCRAAGGTCT	TGGCCRAACG	GCTGATCGCG	CAAACCCCTG	CGCCAGCAC	ATCAKCGCCG	180
AACAGCTGAC	CTGCGCCCGG	ACGGGGGVC	GNCAATACT	CCAAACCCGT	GGCMCTGCTG	240
CTGGCCNAYC	CCGTGTCCTA	ANTCAGAACCT	ASCCSGCNA	CCAKMAACKA	NAACGGTTGT	300
CTGAAGGCCA	GTTCAAAAC	CTCAAGTWCC	GGCCCRACCT	CCCGAAACGG	TNCGAGTCKA	360
TCRSAGGGGG	CGGGGTCGCMC	TGCAACCGT	TTCTCGGTG	GTRCAMCCCN	AAAMCAAGCA	420
TTCCGGGAMTC	CGMTGCGCA	CGCCGCAAS	TTTMCATCGG	GGSGCCNAT	CAAATTGCC	480
GGGAACSGSN	CCMCKTCNK	GGAMACGCC	TWCCAAAACC	CYCGAACGGK	ATCCTTCGKY	540
NAACCGGCA	RCNNCSKST	TCGGGCTTC	NMSGGAATA	CCCKNSCMT	CCGAATCCAA	600
TTCCCMKYYG	CTTTTYYVCC	CCCCGGCCCC	AAAYNGGYC	CCTASSNNMK	KNCCAMNANT	660
CCNWATCTGG	NGGTCCCNAN	KYYGGCGTTC	NMAATSAMJA	NMNRGGGTYT	TSCYACCMNN	720
AACCGKNNKG	CCCCMKCTK	MAAAAKATT	RATCAMKNG	GGNKCKCNCN	NAAMACCCSN	780
CNCYNCWYTC	TMYCKSSKG	GCSMYNANCA	SNGGGGAGGW	GGSGRMKMT	CTMTCTCNCT	840
MGGCCKNNT	TYCKSGAKAT	ACASMNKTCC	GCGCNGCCN	MAAMANRAKA	CTAKCCGYGN	900
CCSNSTMVY	CTSNNMKMN	TCCWMWNATC	NTYYGKCNK	KCTMKATNW	CSCTSKCNCK	960
MRAMTCKTYG	SNNTCCCTCA	TNCNTCKSC	SNMSKNTCK	KSCNCNCW	CNKNMCKCN	1020
GGNSTCRCCY	TCTMNNNTCS	AGCKCGSKNC	WACNCACACK	NGWCTYTTCC	WKNNMCKCN	1080
TKCKCKACRG	MTMTCWCSS					1099

## (2) INFORMATION FOR SEQ ID NO:326:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid

100814843 022503

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

GGNGNTATACA	TCWCTGTGYA	CCSAGGATCW	ANTGCAGCCG	MAAKCTWSTM	CASAGATCTC	60
AAAYTCTCCA	MGAGCCGAC	AKAKYSTCGT	CCMRACCCG	CAYACWCCWG	CNCGCCCGWT	120
CTTRGACCGG	GGKATASMC	ACCGTTGGCC	CCGGCNCGA	CCTACACCAAC	CCACGCCGCC	180
AGCAGCCCCCW	TRAMCAAAAC	ACCCCGCKTT	TACCGCCGCC	CCGGCCGGGG	CCACCAACAG	240
CCCCACCGGGC	ACCACCGGGC	CCGGCGTTGC	CAAAACAGGC	CCGCKTTTGC	CACCRRA	296

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1073 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

NGNGSGNKMY	ATCATCWTTC	TGCACCSNNG	MTCWATTGCG	GCCGCAATCT	TSTMNASAGA	60
TCTCGAATTC	GGCAMGARCA	TCTCGCGGG	GAATGTCCAA	AWGTCWKTAA	CGGCMATCGG	120
TTTGGCGYCA	ACCACKCTRT	SCAKATCGG	GCCAMWTYCA	AACCRATTAT	TTGGGYCGAG	180
AAAATTTCMG	CKTGTTRASCA	ACCTGCGCC	GGTCAASCAA	CAGCCTCTRA	ACCGTAAATY	240
CKTAGGTNKT	YCCGGCAACA	ASCYCRATAA	TSGGGCCCG	AMCCAAAAAA	CCTGANTNGT	300
TNTTNCNRAA	NCCGGTYCCC	GRAGGGGTS	ACTGCGSTAR	GCTTNTWCY	NCCTTRACAT	360
TAAACCCCCC	CGGNTCWTG	CCGGGCGCAA	ATCYTGCCTC	WTKGNCACCA	YCCCANCTG	420
CSGTATGTTG	RAANCASTSG	GCAACCGGT	TGGCTGATYC	KTCGGNTCCS		480
SNAATTCCGG	GATTTACCGS	CAMGGTTAAY	CCAGGYCCCC	TNTGCYTCKY	CNACAAACSG	540
ATCMWCNCCG	TACCTKTAA	AATTCTTGT	GGTGGAAACCC	ANWCKAAAAAA	NMTNTYCCCN	600
TCCAMMGGGG	CYCGGAAKKT	CNAACNTGGKT	NACCCNTNCN	YTGAASSTTT	TCYTGNCCCC	660
GGCCCKAAAS	ANACCSGAKC	CCCGGAAYCS	WTAGGCYTCN	TGCCCCSTTA	AATTKGNCYC	720
AATCCKCCAA	CGCTTCCCGG	GGTCCSSTCM	AAAMTCTCC	CCCKSCASNG	GAATVYCYKSG	780
GCWGTMMATTW	CNCNCNTT	CCYGGNAACAA	SCCCCCWKG	GSTYCCCCN	SNTTSSGCCS	840
GGTTSGAMYC	AAAATWNGGG	MMCNRAGNCG	SGNAMCCSN	GGGGGSATW	TKAAYYYCYGG	900
GGGGGTCNYC	CCRCRCSNAA	AAGYGTCKGC	KCCSSSSCYC	CCMARTTTYT	CNGGMRMCMAM	960
ACCANGGGNG	CTCCCGTNICW	STTCTCCSSN	NSNMAMAAN	NKCKCKGGGS	CKGARRNNMNA	1020
MTCGSNGNGG	WTCCCKNKT	NSCNSGNCGS	YGGNSASWCC	YNYCNCCACA	ANC	1073

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1166 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

CGCCCCGTTTC	TTMMMTTCACT	TCATTACACCG	GGMTCTAGTG	CGGCCGCAAK	CTTGTCKACA	60
GATCTCGAAAY	TCGGCAMGAS	ACAATSTCGG	GTGKGGCAAT	GTCNGGTGGG	GCAACTTTGG	120
GCTCGGRRAT	YCGGGGTTAA	CGCCGGGTCT	RATGGGTSTG	GTTAATATCG	GGTTTGGTAA	180
TGCCGGCAGC	TACAATTTCG	GTTGGCAAA	ATATGGGTGT	GGCAATATN	GGGTYCGCTA	240
ACACCGSCAS	TGGRRAATTYC	GGTATTSGGT	NACCGGTRAY	AAYCTGACQG	GGTNCGGTGG	300
TTYCAATAC	GGTAAACGGGA	ATGTSGGT	YYACYCCCGS	GSAACCGNWV	YTNTNGKTCCT	360
TMMCNCTSSM	CKKSAAMTSM	KMGGTSTYCT	MTYCNNGGAS	TAMTYNMCCC	CGWAYCKSC	420
WAYCCTGCT	CATYCCMCMC	SGSGYCTTCA	MNCCACACYTG	NGYYCCCTCC	MKMTCYCAYT	480
CMNTCCGGTW	CCTNTMMNCC	CSNCNCRYCTC	AMCNCCKSGK	CACCNATMYC	CSACKCHTCT	540
MCYMCSCAKN	MTTCCCTCN	CCTYTNNNCA	CMCNSCTCTM	TCAJACTCKC	CGGGYCKCNC	600
MYCTCTCKCC	AYNNAACCKK	TYCWCWNWC	YMYCKCKCAG	WYKNMCTCCW	ACTCTMYNTT	660
TCTCTCNKCC	CMKACKNNTT	CTWCWSCCCC	TYACCKAYMC	YACNMTMTC	MCTCKACSCC	720
CYYCNYYNCM	NMWCMTWC	TNNAKCANCN	TTCTTCTCTC	MMYMTIMACKC	WCNNNTCNCK	780
SGACCYTCTC	ACTKMKCKM	TCTCTTMC	CCYMWNTCC	MKYNNCCCTCC	NMTCMTCKYT	840
CCTCNCRNMY	CYYYAKACAK	NMTCCCCAN	KMCAKCTKCT	CCCNCAKMS	ACNCCKCCWC	900
CCTCTTATCC	CTYCTCWCY	ATCTCKCTCW	TYCWCWNWC	ACNCKYAYT	CNACTMNWN	960
CCANCNCTCT	CTNYCTCWCK	ACGTYCKCK	CTMKCNYMC	NRWCTYRCCT	CKKCCNCCR	1020
CKNMCMKCTM	CTCTCCWMM	TCCCWCCCAT	CTMKSTCTC	WCNCMTCCCT	CNKCCYNYNT	1080
KCYTYCCMYG	CTTCNCTCMT	MCCWCCYATC	TCTMKCTCT	CWCACYCMAC	WMTTACWNCC	1140
ACTCTCTRCW	CKKCKMCMR	MTCTCB				1166

## (2) INFORMATION FOR SEQ ID NO:329:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

NGNGNNNNNT	CWTACATCWN	TCTNCACCSG	NGMTCWATTG	CGGCCGCCAW	NCTTGTINMAS	60
AGAATCTCNC	AAATCGGAC	ANATGTTCTT	TSTMTAKTGT	GGCGGGGNGC	CACGCCKTAT	120
GTGYGCTCG	GYTRACCCA	CCCCCGGC	CGGGCCRAACC	AGGGGGGGR	TSCAGGGCCG	180
GGCGGGCCG	GCGGYTATAT	RAAGCCG	TTTTKTRATA	ACGGTSCCGC	CGCGGGGTR	240
TTACGGGCA	AAACGGKKT	TTGGGTRTAT	AAACGCTTAAT	GCAACCWAT	TTTYCGGGTC	300
AAAAACGCCG	CGWGCANATC	NCGGGCVNCT	RAGGGCATT	YMCGCCAAA	WTNTGGGGCGC	360
AAAACCCCKT	TSYATTNTT	TGGGCTATSC	GYYGCTTCG	GCAACACGT	CCCCGGTTAA	420
TCCCKTCCCG	GCGCCGCC	AAAACACC	ATATYCGGT	GGGGTGKYCC	CMCAGGCSGT	480
TGCTYCGNGY	CACCTGGCCA	AAYYCCAWT	AKATTTGGTG	SYCKTSCGG	TTSYTGGGCY	540
CAATTACCCC	CNCGGNAAA	GRRAAAANAA	ATTCNCCNTT	TGCTCGGYCA	YCTTTMTTGG	600
SAAAAGGGG	ATGGCSGGT	TYTTTACCT	CAAYCCCCNA	NCANTWACCT	YTCCSCCCGG	660
GGGGNCANAA	CGSTTNGCTC	CGSGGNAAKCC	TKGTMCCCGN	ATCNAAAAGG	CNGAATTGG	720
TYYSSTYCK	ATTWTKKY	CGCCCNWTTG	YAAAAAKK	AAASAKCCCK	YCNCAMMYK	780
NGGGGTYSSG	GCKKNYCTCT	SNMTTAAACC	CYCCCCAAAA	YYNNSGGKKT	TCCGCGYNAT	840
KCCACCNCC	GNNGGGGGNA	AAAAAAAY	TTTYCCSAAA	ATCCCACCCY	TCYKTKSTR	900
AMACCCCTT	TYMMKAYTC	CKYSNATTC	SGMTTCWAA	TYCCYYGGCT	TNTTCCCCCK	960
CSGGNGCCCC	AAWTTTGT	YNCNANTTTC	CCCNAAAMCM	AWTMGGGKS	KCCATTCTGG	1020
SCYTMAANTA	AAANAANGGG	NKTTTYYCTY	MANAAACACN	GTGKCNCN	CNAAMAAAASN	1080
AKMMAAKAGN	KKKMTGNNSA	AAANCNC	CTSTYTNVTT	NKTNMNC	CGGKKNKG	1140
SWSWYNTTCT	NCCCRCCCC	YNYNKTGANA	AAMMN	GGSTMCRNAN	ASNMTTTCK	1200
STSTNGMGC	KMBASNANAN	MCAMWKYCC				1230

## (2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1022 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

NGNGGGKNNNA	TMAYCWTCTC	ACSSGGTCTA	TGCGGCCAW	CTMGTMAASA	GATCTCNAAY	60
TCGGCANNAN	GCATMTCMC	CATATATAAC	CATTGCGTC	GYWTGCAWCT	CRAAWCTGTC	120
CTTCGKCCG	TTKTACRAAG	GTGGMWTGTY	CWTYCCTRAA	SCCCTCRATC	TCCKTKTATYC	180
CTTGGGCTTC	ACTTTAACGG	RATKSCGTC	TTKTYTACATT	RATGCAAWTA	WTGGYCRAWT	240
KTTGCAAGGG	RACGGCWYCT	TTTYCGGCR	GRACAATNGA	TTGGAWYCG	TYGGCRAGGC	300
CCGGCACCAC	ACCGGGCNCC	AAAGGYCCG	GCAAWTSCCT	GGKTCAAAAA	TGGTGCAAAC	360
AAAMCNATCC	CGGGYTRAC	CACAAKACCA	TCCCGTGGCC	GCACCAWNNT	420	
TTYCRATCWY	CWYCCCCACC	TTRAACTGK	YTGCSGTATT	GCCTKCTTGC	CTCRACAGCM	480
YCNCCCTCA	AACCTCGGT	GACTCCAAC	GGTCTGGYCG	AAAGGGGGYT	CAMCGGACAA	540
AACCCCRANN	TCCTNCCCTT	CCYCGGAAAN	GKTGATMTTC	TCNSNAACCSA	600	
CMGGGNNYTY	NAACCCCTGA	CSSSGSNKGA	MYNSCCSGGA	ANTTTTCCCT	TYNGGGGRN	660
AAANCCCTTT	AAGGTACCCC	KGGNGGGKG	CCYYTTGGG	AAAACAACCC	CKATTGGKTT	720
TYGGAAATTT	TKCNCCTTGG	TCNSGGGGG	GGGGCCCCAMC	CCMCMCTTTT	TCMSCNMTYY	780
YCYGGGGAT	TNYTCGCGSG	GAAYYCGGS	CCKGYCCTAA	NCCCCMNWGG	GKYSTGSNAR	840
GGRATMAWWT	TYSTTTYYMC	CCGGCNCCCC	CCCKAKMCNT	KGNTGAACMA	AAAKCSCGGG	900
GSCNMMYWWY	YCNNNNGNRTT	TNRGSSNMT	TYMAAMMAN	GGGGKYWYY	CKCCNGSCNN	960
GKTYSGGGST	TTTCCTNTTS	GGGSSATYKG	MACCCCKTMT	AYCGGGGGT	NTKTKYCCCC	1020
SC						1022

## (2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1083 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

NNCGNNKNNTA	TAMAYCWTYCT	NCACCSGGGA	TCWATTGCGG	CCGCAATCTT	STMAASAGAT	60
CTCKAAYTCG	GCAMGANCCG	CAWCTATTG	KGTGRASCGC	ACCAAGCGRGA	CCTCGCSGKT	120
CKTTCCTTGC	AGRGAAGCC	TGGGTGGCR	CGGTGGCAAT	GCCAACCGCC	CCCCAAACACN	180
CCGCAAATMY	CRAAAACAA	CCCSGGGTA	GKTCCSGGGC	GCCAATMMA	TAACCGTKT	240
AACKCAGGCN	ACGGCCAAAC	GGYCCGCC	AACCAAGCNA	CCTCCCCSCC	NATAGGYCCG	300
GTGGGGGCTC	CCTKATYKCC	AACSTCGTC	CTCNAGGGM	CGGYCCMWT	TCCGCTCTCAT	360
CCTGCTCTTC	TTMMATTTTC	CRTECACYKG	CGGGGGAAACY	TTTTTNYCNC	CCTTGSCMAN	420
CACCNAAAGY	CNAAAATTNC	CCMTGCKY	SNNCAAAAGR	GATTGGGGTY	CGKKTTTTNT	480
TCTNMCMAAC	CNCNNNTNA	CGCCNNTM	CCYTWTACCC	CCCWWMCMNS	ANGKTTGNSA	540
AAKTNCCCCC	AAATRCAAA	MTTCTCGCC	NTTTMTWMCY	YCCCTTTCCC	CMCCCNWNAA	600
GGSCRCYYY	TCGGGAANTY	TCCCCNAAA	AWTCAMWCCM	TTTCCCNCCA	AGAAWTTCSG	660

SACTCCTTNTT	TTCNGGGNAM	ATANATYTTT	YCKTNGGGSK	TTCCGGMTCNC	AMMAATNTCC	720
RGGGKAAMCC	AGKNTNNNTCC	YYYYCCCCAA	NNTYCCYKG	RMCYNNYYCY	TTAAAANRASR	780
SAACCCSKGG	GKCYNCNCSS	TARCCCCCAM	KAAAATTTCC	CCCSKTTTC	TYNNNKMRW	840
GCCCCCSAAM	ACTMTWAYTT	TCCCCKGNNN	TTTSYCCKCS	KCAMSMMWMTG	KRNCTTTTTT	900
YCSMATAAMA	CTTNGGKCCCT	NTCNYGSGCG	CMAAANAAGG	CGCGSTTCCTN	TTCWMMAMACA	960
YNTSGNMMMA	SAAKAKWATA	AWNNTRKYK	TKNNCCCNCC	CKCKCTTSNN	TNKCCMCSKS	1020
GGGKNWNKKR	GWCTCCWCNC	CKCCCNKKNK	CCKWATMCCC	CCCCSKCCGM	NCMMNTTCK	1080
CCC						1083

## (2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1069 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

GGGGNNKYAT	MCAYCWTCCTS	YACSGGGMNC	TATTGCGGCC	GCAWYTNGMT	GASAGATCTC	60
GAAYTCGGCA	MGAAAAAAGW	GATGTCCTGG	ACCTTMMCCC	GCGGGACGCR	ACCRACAAAG	120
RAASCGGGCC	ANAAATATTCG	CCACACTTGG	TCACATATTTC	ACCCAATTMT	AYCAGGAYAT	180
MCCATTCCKG	GGACCRACCG	CACAATCCCR	ATSKTGGTTT	GCRAACCCTR	ACCGTCCCCA	240
MYTYCGCCRA	STTNGAACAG	GGCRAAAAAA	CTCGGCTTANY	CTCGCCCTGA	NTCCCGCTCS	300
GCGCNAATAA	CTAGGCCCAT	TKAACGGAAG	CGGNNGCCSC	NANTTGGCCA	ACAGGTCTTR	360
ACAAAGGGC	CCCAASYYCGG	CCGGWTCCW	TTYCACANCCC	TNKTCCTCTG	CCGAATYCGG	420
WTCTCRATNYC	CCWTGGGCCT	TKTCKYCYC	TKYCGGNTCCA	AWTCTNGGT	TNCTATRKGK	480
TCCCCCTAAAT	SCANATCTCG	GCKYCCATT	NTCTGGSNTTC	NATTTFAMMAN	SRRCGGTTCT	540
TTCWTTCCRA	AACCGSNTGG	GCCCNMMCCA	AAAATGATN	ATAATAATGK	YGSCTTTCAA	600
ACCCCGCCCC	CCCATTCRWT	CSGTTCTGAC	CCCCNGNGGT	TAAGKTGGGA	ATTYYTNAMC	660
YCNARGCCCC	NATTTSGGNA	AAAACCYYCY	GGGGYCTCAA	CMNYTTTTT	GSKSSNTCGG	720
GCTCRTTCS	CARAACCCAA	ATTNTYNYGG	GGYCCKTNAA	ACMCGGYCRC	RCCGGAAATT	780
TTTYTGGTTC	AACCCCAACCC	TTTCAASCC	TTTCTTYYTT	TRCCSSCSMN	TNGSSGGNT	840
KSSCCNTTCY	RARKKCCNMM	GGGGHWYCYN	CCCCRMNTT	CTTTTTTTT	CCGTINNMAAM	900
NGKTTCTTC	AASMCCCCCC	SCCCCCNSAA	ACCCCTNAR	GTTCYYCMA	AANNWYNNGN	960
KNCCCCCCCC	MMNAAAAY	YCSCCCGNRR	ACMSNSNGGA	MCCCCGGSN	NTTRKTTTTT	1020
TNCMSGYVCCC	CSRMASYYTT	TKAMANMANR	GAMMNSMTTY	TNNRGNWNK		1069

## (2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

NGNGGGGKWK	MATACATCWT	TCTTCACGSG	GGATCWTATTG	CGGGCCGCAW	TCTNGTMCAA	60
SAGATCTCGA	TYTCGGGCA	NACCCACWC	TCCRAAAAAA	ACCCRAAWCT	CGGGSKCTYC	120
GARAAGTGT	GGCCGCKTTR	ATTAAACAA	ATTCACTGTC	ANAGTGTAC	GGCKTTACWT	180

YCCCGGCAAA	GGGGCCACAA	CCTGCAGRGA	SCACYCRATG	GKTGYTGKTS	CNCGGGCGGG	240
CCGGKTNAAAG	GGACCTGCT	GGGTTGCGC	TMCAAANATC	WYCCGGGGT	YCGCTGGRAT	300
MCNCAGGGGT	GTCAAAACAC	CGCAACAGG	CACSCCANCC	NTTACGGGS	CTTAAAANGA	360
AAAAGGCTG	ATGCCCCAA	GGGGGCCCG	NCCCAACCTT	CGTGTGGTC	ACAACCCGGT	420
CTCTCKTGCC	RAATCCGRWT	CCRATNYNCN	CWTGCGCTT	TCKYCTYCTY	CGGTACCCAA	480
ATCTGGGTAT	CCTATASTGT	CCCCTAATWT	CCAATCTGG	GCTGTCCATT	TSCITGGCNT	540
TCCAAATTAA	CCANCAACGG	TTTCTTNCAT	NCCAAAACCC	GNTKGGCKCC	NRACCCRAAA	600
AAATGAAATAA	TAATAANNGG	KCNNTYCNA	ACNNCCCCC	GTNSGTTCCA	TYNSGTTCCA	660
NMNCCCCCAG	NGGKTAGGTTK	GGGAAANYYC	TCMACCCYCA	ANCCCTWARS	TTTTNGRAAT	720
KAAACCCCTYC	YCNGGGTCW	TYMAAAAAMA	NTTATTGGN	NGNTTTGGG	MWNCKRKNST	780
SCCAAAATCC	MAAATANTTT	YTGTGTYCNA	WTAAAAMCG	YGNCCMNCCC	GGAAAAAWTT	840
TTNTGKTTSA	ACCCAAAAC	YTNTTCMNA	NCSSKTTTT	CYTTCCCCCC	AMNWTTGGGYS	900
GGGNATKGYG	SCYNTCTTA	TKTKYTYMTW	CMGGGGGGNN	MKMTCMCCCC	CMTTTYYCY	960
NYWRRTTTT	CCCCCNKMR	NNRAANNGGN	YTCSYNAANAA	AAGCNCCCCC	SCCKNCCCN	1020
AAAAWCCCCN	NNNARAKTN	TTMKKMRNN	SCCKNKNKGK	YCCCCCCCWC	YNNNNAAAAA	1080
AATMYCCNCC	RASANMCASM	NMGGGRNRS	CCCCCCCSTT	NNNNTMTNT	TTTTTCSRA	1140
GAGCKCCSCG	MNNANMKNC	CTTTTKCNC	NNGNNGNGNN	GGNGMNCCKK	CCNAGAAMWK	1200
CTKSTCCCKS						1210

## (2) INFORMATION FOR SEQ ID NO:334:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

NGSSNNGNNA	TMCATCWYCT	GYACSGGGMT	CWATTGGCG	CGCAACTNGT	MAASAGATCT	60
CGAAYTCGG	AAKANACACC	ACCGCGGTGT	MTATACACCG	CAAATGTTCT	GTKTGCAAA	120
ACCGAGACGC	GGCGGGCGCC	GGGYTCACAC	GCKTTACATY	ACCCGCCAGY	TCAGTGTTRA	180
AACCGTGTY	RAGGGCGGCC	CACCAACTWA	ACGCTTAAK	CAAGRAWYTG	GKTGGCCCG	240
AGCCACCTGY	TGTGGYTG	CTCWYCGGTG	GTAGCGCCGG	TTANCGCCG	TTGCGCYT	300
AMCASCSCG	CGCTTATC	AKCNWTC	CGGCGMRA	CACCGGGC	TTGGRACGCT	360
GCCGCAATT	CAAAYCKYCT	GRWTCTTC	AAACACCR	AAGGCCACCM	CCMSCACNA	420
ATMGGRACT	TTAAGGCCA	GGCAAAACCT	NTRAKCNCT	CCGGGCRAA	GGTCCSGCAA	480
SCRATCMAA	AAAACCKNAT	TTCCCGGAC	ACGCAACCC	MMCGSTTTGC	TGCTTCCGGA	540
TTCGAAMCCA	ATTMCWGKG	NCNWGGGAA	AAACSCNNCC	NWTAKCMGG	CCCMCGGGCA	600
ATTCGSRCA	SAACCCCTNY	CCCGGGTTT	YCTCTGCTCG	GCCCAANACC	CCCGGGAA	660
AAAAASGGT	GGNCAAANGG	GCMAAACCCS	SACCOMACTT	WTTCRCTTN	GGGGGGGSCW	720
CCKNGTTAA	AWKSCCTCY	CTSCCAAA	TGCKMMAA	NNGRKTTGGK	TTNGGCNAC	780
NTTCCGGKC	CCGGGKGKGK	WGKYCTMNA	CSTTNTTTT	SCCCCYKAAA	NYSCCCCCC	840
CGGSSCCCG	CCGGGGGGGA	NNTTTTAMA	GKTYCCCT	CCCCAMAAAA	ANACCCCN	900
CCSGGSCCT	TTKRWAAMN	KCTSCCCNG	GNNGGGKCM	GGKTTATT	NNNCSCCCCC	960
TCCGGGSAAA	AAATAKMTT	SYCCCCCN	CTCCCNKRN	GKAMMSMC	TCCCYCTCN	1020
GCNKNTWAAN	ARSNCKKNN	CCNCYCKCGS	NSNGKCNWCD	NCCSTSNNT	NKGCKNCN	1080
KAAAANAYNC	NGMSSTSSM	CNKKC				1105

## (2) INFORMATION FOR SEQ ID NO:335:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

NGSNNSNNNN	TAMAYCWYYC	TSCACSGGA	ACWANTGCGG	CCRMAWCTNS	TMKASAGATC	60
TMGAAYTCGG	CAAGAGCGGC	AAAGAGTGTGT	GCATCTGGTC	ANAGTSTTMA	CRGGTGCCG	120
CGGGTCKGTR	NTTGGCRACAC	CAAACCCCTTC	GGCGGYCACC	GGCKTGGCC	180	
GCAAAWYCTT	CCAGGCCACC	TCRAACAAWY	YCTCTGCAA	CGCARGCCGT	TYCGCCGCCG	240
RATCCCTGGKT	CASYYCGGCK	TGCGGTGCC	AAAGKTACTGG	CSCAYCAA	CCGCTCGGG	300
RAACRAACTT	AWATYTGGCG	ATTTCNTTC	CCCTGCGGCT	TGATAAATT	NTNAAGCCAC	360
CGGAAAMCTY	CGGGCKTCTC	CTCKTGCRA	ATYCGRWTCC	RATAYCGCA	TGGCTTNKTC	420
KYCTCYKCYC	GTACCCAAAT	CTTGGGTATC	CTATANTKTC	CCWAAANRCA	AWTCTGGCK	480
KTCCATKTS	TGGSKTCRCA	ATTATMAMCA	NCGGTTTCTT	TCWTACCAA	AACCSNTGGG	540
CCCCRACRCA	AAAAGATAAA	TAATAAKGTT	CNWVCAAAAC	CCCCCCCCCC	RRTTCAYCG	600
GTCARACACC	CCANGNGGTN	AGGTNGGAAT	TYTMAACCCC	CAGCCCATAA	SNITNSGNAA	660
AAACCCCCCN	GGGYMYCAAA	AMMCTTTTG	GGGMMTCSGS	CCATKGYKCC	AAAACCAA	720
TMITTCYGT	CRWAAAACG	GGCCNCNCGG	NAAATTTTT	GKCAACCCCA	AACCTTMM	780
CCNNNTTCYY	YCCCNASCAA	TNGGSGGNK	NGSSCNITYT	TWTITTYNNA	GGGGGRWNC	840
SNCCCCNAAN	YCCNAANKG	NKCCCGSNMA	AAAGAGANIT	YCMKAAAAC	CCCCNCNC	900
NAAYACCCC	MAAKWTTCM	AAASMSCNNG	YCCCCC			936

(2) INFORMATION FOR SEQ ID NO:336:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1042 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

NNNGNKNNNN	ATMMAYTCWY	YCTSCACCSG	GGNNWCWATT	GGCGGCCRMAW	KCTTGTMAAS	60
AGATCTMNAA	YTGGCACAG	ASSGCACAG	ASCCGGGGG	CTATCYMCC	GYTGCTCATG	120
CTCAACACGC	TKTKTCGGCG	GRATAATGGC	NCGCCGGCG	CGCCRAACAGC	YTCAAYTGTCT	180
TCGCCAACGC	CATATNCCTAA	CAAGGTRATA	AAASCAAAC	CGCSCGGCG	GCCCCTTGGC	240
SCGGRASACG	GTGCGAACCTT	RAAACNCCKT	GGGCACACYCG	KTSRACTTTA	AASGGTAATC	300
TCKTCCTCT	GGGCTATGGT	GGGCCACAAA	CCTSYTGGCG	WGGGTTCTGGC	CCTGGGYCAC	360
CGYCRNCNTT	TATNTNTCTCK	YCTACACNCCT	TKGGTYCAAC	CAACCCACTT	CACMAAATTG	420
TTTGGGKTG	GGGSSGCGG	YTGTNNCCGK	TAATAATCSG	NTGKTCGCGC	MYCACCGGWA	480
CCATANCCTG	GCGGCCSTG	GCAAATTTC	SAATCATYT	CCTTCTGRAC	CCCCACAMRC	540
CTNSAAATCC	GRATCAATC	CCCNKGCGCTT	NTCYCTCTCN	GTRCCCCAATY	TGGTTTCTAT	600
RKTNCCYAA	TSCAATTGGS	TTYCCRTTSC	YGSTTCCAA	TTNACAAAM	GGTTTYYTCT	660
ACCAAAACCC	NTGGSCCNNA	CMAAAAAKNA	RAAAANAKGG	KCTTYYAAC	CCCCCCCTAT	720
TCAWYCGGTH	CMRNWCCCC	NGKAAGGKG	GAAYAYTHRA	CCAAANCCTMT	ARSTTSGNNAK	780
AAACCCYCG	GGGTTSMAAA	MKNNTWTTSSC	CTTCGGMCTT	YCCAAATMSA	AAATYTCCK	840
KRMNAAAAMC	YGNCCCSAA	ANATTTTGT	NAAMCCCKMA	YYTRTTWMC	WTTTCCYCC	900
CCMCCNNNSG	GNTTCCCTTY	TYATTTCYMM	MCRNNSGACN	CCCCMNTT	TWTTCCKWCWN	960
MMARGSNNNYT	RGRMMNNMCC	CCNCCCCNAK	MTCCNCAA	NTTTNAACNN	NNKYCKCCCC	1020
CCCMWNKNC	CCCCNCMTT	TM				1042

## (2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

NNSGSGMKKK ATAMATCWCT CTSYACCSNG GMTCWATTGC GGCGMAWTC TNGTMAASAG	60
ATCTCGAAYT CGGCAAANAK ACGCMAYGTC AAGTGTTRAYY CGGTCACATA TCMTCGCGNG	120
TCAACMCCA AGCCGNGTCA CCGYCTCCCT GGGGCGCAC CCCCATCGGT RATGCAACYT	180
CGCGCGCAC CGYCAAAGG KTCWTTTRAGG CGCTAAAGGT CAMCAATTCC TRAGGTYMCN	240
CACCGTTNTG TGGCGCCGG RAWTYCTRAC CGGCTAAWTTC GGTAATCGRG AATTGGGCW	300
YCGGCTTGGG CAAATAAGKTN TTGGGCAACG GCGGRWTCYC NCTGGCGRG ATTCCNCAT	360
TCKKTTAACG GKTGRACCGT TTYYCCGGYT GCGCTAAAYT YTYCNTGGG GCCYTCGGCC	420
CRNAGCASY CRCTAACGGY CMCCAGGCA TACKTGTGGC TTTRAACACAC CGGRATNAAY	480
TGKTAACCAAC YTCAAASSGTS CTGRANITRK TNTCNTGAA AANMCCACCN AACCCGGNT	540
RATCTGCTTC MTCANCWTTT SCCCGGTTCT GCGCTTTTG AAYCTTNATC CMTYCAAAG	600
GTTTAMTTT CCAANRAATT CGGYTTGCCA CCTTGGCCGS GGCTGGTTIM CGMWCCTRR	660
AMATCCNCNS GCGGGSAAAN AMTTSGGNT SGSCCGGTCC CCCGNAATAT YCNTPGCCT	720
GNAAATGTSS GGGATCCCN GGSNAYCCGG CTCKWKGGGT TNCCCAAGTTC GWACAAATTG	780
WKCGCTTCC AACCAGGGCC CGGGGGTGG GSCCCNNTT CCTMYNNAAA AAGKGTITGN	840
NYTTTTCCG CNRAANTTCA CCSKCNKNTT GGNCCNAACY YYYCAANTC CANACCTTA	900
AASAAAANCYK YGKTYVCCCC TTTTCCCGS SANCCCCCM NMWSKNCGGG AAAAAAAGNK	960
TYNGCCTTAN CNSKNTKTTN TNKTYCCCCC NMWNNSNMCY NCBEKKCNKRY NGNSNMNCCT	1020
MKYSKCNNNN SNNNNNNKCGN GSNCGSMKYM CMNNCNGMYK NGNKSNNCCC MSC	1073

## (2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1061 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

GNSNGNKNNTN TMCAYCWYCT SCACSGGGTC TATTGCGGCC GCAATYNTGT CKASAGATCT	60
CGATYTCGGC AMNNAARTG TCGTCGTCAA TTTCAKGKKTG GTCKTCAAAY GGGCCAGGGC	120
GNGACCRACA CCTCTGNGTCA CCCAAAANAK CAACAGWCTC AATWTCAAG GCCRAGGSC	180
TRTCATYTCR CRASCAKTTA ACCGTYKTCW TCRAAGGTGCG ACRAACAGGC ACCCAGYTC	240
CCGCCSGGC AWTCGCGCTG CGGGCGGTN TCAGCGTGTAT TYCTGACCCCT RWTCGTSGG	300
TGGYCACTNCT GGTGTAAGGCC CWWCCGNCNA AGAACTGAGG GGCRAAATTCC CAGGANCNNA	360
GRAACCCNAG GAAACCGCCG TAKAACCCGG CRAAACCRAG GCGCTGTGGC ATTCCNATTA	420
NAMSGGTTTG CRACNTGGCC RAACCGTTT CTTGGTCGGC CTCGGCAACC CTGGACCCANT	480
TACCCCKTNC CGCGNCCNMAC CYCGGGTNTCT TGKYCAATAT NTGCYCCCCCG GNRANTNGGC	540
CNAATTCCAG GGCNCCNACT TTCCGGCCCN AATTCCCYTG GTTAATCACC GGGCNCNCCT	600
GGTTTGGGC AACCCCNCSY CTTMTTTAAA CATTCCGSCC CAAATGGGNC STTGGSAAAT	660

TCTNTYCGGT	GGGGCGSGCR	ANMYTCTCT	YCCCNAASAN	CTTAMYCCAN	TCGSSNTCC	720
CGGKCAAWS	NGGGGGGNGA	AAGGGCCCC	CGGNTSKCC	GGGGKGCCC	CYGGKTTCAA	780
AANTTTCGCG	GKTSTMSCGG	NVTCSCCCC	CSGCCAAGRA	CCGNGGTTT	TTTTGAACCC	840
KCMANTCSSA	AMCCGCCSSC	CCCMMAAAGGS	GCCTNAWGR	RAYTTNKSCC	CNAAAACS	900
CCCCCAKYTY	SGGKTTCNNC	CNCCSGKKG	CCMTSTTTMM	MRCCTTTGN	GNKTTTTTAN	960
MGSCTTNNC	CACCCCCYCK	GGGCKSMNNA	GAAKTMWYK	CNGGGNNAN	RSCCCCCNN	1020
GSGKGGGGKG	MGAGYSCCKT	CTKGCGNCNN	YKNTTCCCC	C		1061

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 986 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

GNNNNNNKWN	ATMCAYCWY	CTSCACCGG	GMTCWATTG	GGCCGCAWKY	TNGTMAASAG	60
ATCTMGAAYT	CGGCACANAG	CGGCACAGAG	TGTGTCATC	TGTGTCANAG	CTGTCACACGC	120
GGTGGCCGCG	GTGGTCCG	CMCATTCGGR	AACACCAAAC	CCGTCCGCGG	GYCACCGGCK	180
TCGCCCTGCA	AAYCTCTCAG	GCCACCCYCA	AACACAAYWCT	CCTGCAACSC	ARSCCGTTYC	240
GCGGGCGRAT	CCTGGKYCAS	YTGCCKTGC	GGTGGGCCAA	GGTACTGGCS	CWYCRANACC	300
GCTYCGGGR	ACCCNAACGTA	ATACCTGCGN	AAATTGCGNTT	CCCCCTSCCC	TTRATNAATT	360
TGTTAAACCA	CACCCAACTY	CGGGCKTCTC	CTCKTGCCR	WTCCGRWTC	RATNYGCCA	420
TGGCCTKNTC	KYCTYCKYCS	GTMCACAAAT	CTTGTGATTC	TATATTGTC	CTAAATGCAA	480
ATCTKGGCTG	TCCATNTGCT	GGCGTCTCAA	WTWAMANAG	NGGTTTCTTY	CTTCCNAAAC	540
CCSTTGGCC	AAACCCNAAA	AAATGATNATA	ATAATGGTGC	TNTCAAACCC	CGNCNCATY	600
CNATCNSGKCC	AMMCCCRGNG	GGKTANKKG	GNAATTCTTM	AACCCCAAGC	CATAASNTTG	660
SGANAAACCY	NCNCMGGYCA	CCAAACACANY	NTNTTGCNGY	SNNTTCGGMN	YCAGGCTNN	720
CMAAAACCCY	AAACTCTNYY	GGYCCAAATA	AAMMMSGGYC	SAMCCGGAAA	WTTTTYTGN	780
KYNAAACCCA	AAKCCCTTTT	CNAACCCDAN	WNTYCTCNCC	RCRMANNTGG	CNSGGARTTKT	840
SSSCTTCC	ATGKYCCMMA	AGNGGGGRNA	CCARCCCAA	TTCCCTNNNTN	KNKNCNCNST	900
TRNAAAAGGG	GKNTYNCMAA	AASCNCNC	NCNCCTCCAA	AAKAMCCCC	AAAGAKNTCN	960
NAANASKYSN	NNNSCCCCC	CCMMNN				986

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

NGNGGGNKRN	ATMMAYCWCT	SATYYACCSN	GGMNMWATTG	CGGCCRMAWT	CTNGTMKASA	60
GATCTMGAAA	YTCGGAAAG	AGYATKTCG	GGGGCAGAT	TTNTGGCCCG	CAACCCGCGC	120
ACTTTGCAWY	TCACACATCC	SGGTGCCCCA	AAAATWCT	ACCCCCATMC	TYCKTGCASM	180
ASYTGCGCCC	RATTRAACAC	CCGGCGGGCW	TGCTGGCCCA	GGTATTYCAS	CAGYTCAAAY	240
YCTTTKTAGK	AAAAATCCAG	CGSGCGGCCA	CNCAGCGGG	CGGKTAGGT	GCCTYCRTCA	300

ATMACCAGCY CGCCCGAGGY CACCTTGGCC	AAAAYCTCT	GGGTCA	GCA	ATTYCCGS	360
CCGCCAACM ACCANCGCA	TYCTGGC	NTC	AATCYCACCG	GGCCGGTGY	420
GRATCTCKTC MANCCCCAN	TCAGCSY	TNA	CNGCMACAGC	CGCCTTCTT	480
RTACCGGGWT	CAACCGCCS	GTCA	AACTCA	ACAGGCGNC	540
GTCTTACSCC	NNYA	ANAAAAA	MAAGNTCTGT	AGGCC	600
CGGGCCTCN	NM	GGGG	TTTG	CTTC	660
CAAGTCNCMT	TWAWA	ACYCN	NNAACCCCCC	CASA	720
TTTASGKTS	GGGMMY	YCTY	TTAAAAAA	AAAG	780
GGNAAATT	CAAM	CN	WGK	NTT	840
CSSGSNNNAT	TAYGG	MSNMT	TTTNA	AWTM	900
TNAMCKCCN	CCTC	NGK	NC	NSAM	960
CGGA	AMCMN	AAT	CGGAS	CMN	1020
CCNSNSGMN	RGA	ARM	TY	YCCCCGSKM	1074
GGKNA	AAAW			GKYCCCC	
				CC	

## (2) INFORMATION FOR SEQ ID NO:341:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

NGNGNCNKNT	MTACATCW	T	CTGCACCSGG	GNTCWANTGC	GGCGCAW	KY	TTGTCGASAG	60
ATCTCGAAYT	CGGC	ACGAGG	ACW	CTGCGRA	CGCC	CCCC	CACA	120
ATTGNGCCK	TCAC	CGGCC	CG	AYTGANC	TNC	ACTG	GGG	180
GGCC	TAC	CGC	CG	RAAGG	CG	CG	CGC	240
AAAWTGGCCA	GCG	GT	GGC	TG	CG	AC	CC	300
AATCCGGYCC	NTC	TG	TC	ATGG	TC	AG	CC	360
TCGA	ACTTR	TC	NA	AACT	TG	TC	ATG	420
TT	CNGW	W	CG	GC	CG	CC	GA	480
KGG	AAA	AG	RRC	CTA	ATG	GG	GG	540
GAAGG	C	CS	MA	MTY	GGT	CC	CG	600
NNK	MW	ITK	T	CRG	NGG	CC	CC	660
SAAAG	NTK	CS	TC	AT	ST	CC	GG	720
CGAA	WKR	W	CC	Y	TG	AT	GG	780
TYT	NKG	GAC	W	SC	CC	NT	TT	840
TAAG	AGG	GAG	CS	NC	CC	NT	TT	900
TAT	TKM	KG	CG	CKT	GG	NC	NG	960
GGG	NTT	TGT	TA	GAT	TC	TC	TC	1020
MNN	SKT	MMT	MS	CKT	CG	CG	CG	1080
GGC	NC	GMN	MG	CS	SS	CC	CG	1140
GT	CNG	CGC	CG	CG	CG	CG	CG	1195

## (2) INFORMATION FOR SEQ ID NO:342:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

CCATCTGATC	GTTGGCAACC	AGCATCGCAG	TGGGAACGAT	GCCCTCATTC	AGCATTGCA	60
TGGTTTGTG	AAAACCGGAC	ATGGCACTCC	AGTCGCCCTTC	CCGTTCCGQT	ATCGGCTGAA	120
TTTGATTGCG	AGTGAGATAT	TTATGCCAGC	CAGCCAGACG	CAGACGCC	GAGACAGAAC	180
TTAATGGGGC	CGCTAACAGC	CGGATTGTC	GGTGAACCAA	TGCGACCAGA	TGCTCCACGC	240
CCAGTCGGCT	ACCGCTTCA	TGGGAGAAA	TAATACTGTT	GATGGGTGTC	TGGTCAGAGA	300
CATCAAGAAA	TAACGCCGGA	ACATTAGTCG	AGGCACTTC	CACAGCAATG	GCATCCCTGGT	360
CATCCAGCGG	ATAGTTAATG	ATCAGCCCR	TGACGCGTTG	CGCGAGAAGA	TTGTGCACCG	420
CCGCTTAAAC	GGCTTCGAGC	CCGCTTCGTT	TCACCATGCA	CACCAACAGC	CTGGCACCCA	480
GTGATCGGGC	GGGAGAGTTA	ATCGCCGGCA	CAATTGCGA	CGGGCGTGC	AGGGCCAGAC	540
TGGAGGTGGC	AAAGCCTAAC	AGCAACGACT	GTTTCCCGC	CAGTTGTTGT	GCCACGGGT	600
TGGGAATGTA	ATTCCACTTC	AGCATCGCCG	CTTCACCTT	TTCCCGCCTT	TTCCGAGAAA	660
CGTGGCTGGC	CTGGTTCAAC	ACCGGGGAAA	CGCTCTGATA	AGAGACACCG	GCATACTCTG	720
CGACATCGTA	TAACGTTACT	GTTTTCACAT	TCACCCACCT	GAATTGACTC	TCTTCCGGGC	780
GCTATCATGC	CATACCCCGA	AAAGTTTTCG	GCCATTCGAT	GGTGTCCGGG	ATCTCGACGC	840
TCTCCCTTAT	GCGACTCTG	CATTAGGAAG	CAGCCCGATG	GTAGGTTGAG	GCCGTTGAGC	900
ACGGCCCGCG	AAAGGAATGG	TGATGCAAG	AGATGGCG	CCAACAGTCC	CCCGGCCACG	960
GGGGCTGCCA	CCATACCCAC	GCGCAACAA	GGCGCTCATG	CGCCGAAGTG	CGRGACCCGA	1020
TCTTCCCAT	CGGTGATGTC	GGCGATATAG	GGCCAGCAA	CGCACCTGT	GGCGCCGGTG	1080
ATGCCGCCA	CGATGCTCC	GGCGTAGGATC	ATCGAGATCT	CGATCCCGG	AAATTAAATAC	1140
GACTCATACT	AGGGGAATG	TGAGCGGATA	ACAAATTCCC	TCTAGAAATA	ATTTTGTTA	1200
ACTTTAAGAA	GGGAGATATAC	ATATGGGCCA	TCATCATCAT	CATCACGTTGA	TCGACATCAT	1260
CGGGACCGAGC	CCCACATCT	GGGAAGACGC	GGGGCGGAG	CGGGTCCAGC	GGGCGGGAGA	1320
TAGGGCTGAG	GACATCGCCG	TGCTCTGGGT	CATTAGGACG	GACATGGCCG	TGGACAGCGC	1380
CGGCAAGATC	ACCTACCGCA	TCAAGCTCGA	AGTGTGTC	AAGATGAGGC	CGGCGCAAC	1440
GAGGGCTCG	AAAACCCAGG	GGCGTTCGGC	TAAACAGGGC	CGCCGGCGCG	GTACTGTGCG	1500
GACTACCCCC	GGCTGCTGCG	CGGTGACGTT	GGCCGAGACCC	GGTAGCACG	TGCTCTACCC	1560
GCTGTTAAC	CTGTTGGGTC	CGGGCTTCA	CGAGAGGAT	CGGAAGCTCA	CGATCACCGC	1620
TCAGGGCAC	GGTGTCTGGT	GGTGTCTGC	CGACGGCGCC	CGCCGGACGG	TCAACATIGG	1680
GGCTTCCGAG	GCCTATCTGT	CAGGAAGTGA	TATGGCGCCG	CACAAAGGGC	TGATGACAT	1740
CGCGCTGAGC	ATCTCCGTC	AGCAGGTCAA	CTACACCTG	CCCGGAGTGA	CGGAGCACCC	1800
CAAGCTGAA	GGAAAAGTCC	TGGCGGCCAT	GTACCAAGGGC	ACCATCAAAA	CTTGGGACGA	1860
CCCGCAGATC	GCTGCTGCTA	ACCCCGCGGT	GAACCTGCGG	GGCACCGCGG	TAGTTCGCT	1920
GCACCGCTCC	GACGGGTCTG	GTGACACCTT	CTTGTGTCACC	CAGTACCTGT	CCAAGCAAGA	1980
TCCCGAGGGC	TGGGGCAAGT	CGCCCGGCTT	CGGCACCCAC	GTCGACTTCC	CGGCCTGCG	2040
GGGTGCGCTG	GGTGTAGAACG	GGCACGGCGC	ATGGTGTGAC	GGTTGGCGCC	AGACACCGG	2100
CTGCGTGGCC	TATATCGCA	TCAGCTCTCT	CGACAGGGCC	AGTCACGGG	GACTGGGCGA	2160
GGCCAACTA	GGCAATAGCT	TGGCGATCT	CTTGTGTC	GGCGCAGAAA	GCATTCTACGG	2220
CGCGCGCGGC	GGCTTCGCTA	CGAAAACCCC	GGCGAACACG	GGGATTTCGA	TGATGACGG	2280
GGCCGCCCG	GACGGCTACC	CGATCATCAA	CTACGAGTAC	GGCATCTGTC	ACAACACGGCA	2340
AAAGGACGCC	GCCACCGCGC	AGACCTTCTCA	GGCATTTCTC	CACTGGGCGA	TCAACGACGG	2400
CAACAGGCC	TGCTTCTCG	ACCAAGTTCA	TTTCCACCGC	CTGCCGCCCG	CGGTGGTGA	2460
GTTGCTGAC	GGGTGATGTC	CGACGATTTC	CAGGGCTGAG	ATGAAGACCC	ATGCCGCTAC	2520
CCTCGCGCAG	GAGGCAGGTA	TTATGAGCG	GTATCCGGC	GACCTGAAA	CCCAAGATCGA	2580
CCAGGTGGAG	TGCGACGGCA	GTTGTTGCA	GGGGCACTGG	CGGGCGCGG	CGGGGACGGC	2640
CGCCCCAGGCC	GGCGTGGTGC	GCTTCAAGA	AGCAGCAAT	AAAGCAGAACG	AGGAACCTCGA	2700
CGAGATCTCG	ACGAAATATC	GTCAAGGCCG	CGTGGCCATAC	TCTAGGGCCG	ACGAGGAGCA	2760
CGACGAGGCC	CTGCTCTCCG	AAATGGGCT	TGGATTCA	TTCCGCTGTC	CTGCTGGCTG	2820
GTTGGAGTCT	GACGCCGCC	ACTTCGACTA	CGGTTACGCA	CTCCTCAGCA	AAACCCACCG	2880
GGACCCGCCA	TTTCCGGAC	AGCGCCGCC	GGTGGCCAT	GACACCCGTA	TCTGTCTCGG	2940
CGGGCTAGAC	CAAAGCTT	ACGCGAGGCC	CGAAGGCC	GACTCCAAAG	CCGGGCCCG	3000
GTTGGGCTCG	GACATGGTG	AGTTCTATAT	GCCCTACCG	GGCACCCGGA	TCAACCCAGGA	3060

AACCGTCTCG	CTYGACGCCA	ACGGGGTGTG	TGGAAGCGCG	TCGTTATTACG	AAGTCAAGTT	3120
CAGCGATCCG	AGTAAGCGA	ACGGCCAGAT	CTGGACGGGC	GTAATCGGCT	CGCCCGCGC	3180
GAACGCACCG	GACGCCGGGC	CCCCCTCAGCG	CTGGTTTGTG	GTATGGCTCG	GGACCGCCAA	3240
CAACCCGGTG	GACAAGGGCG	CGGCCAAGGC	GCTGGCCGAA	TCGATCCGGC	CTTTGGTGC	3300
CCCGCCCGGC	CGCCGGGGCG	GGGAAGTCGC	TCTTACCCCG	ACGACACCGA	CACCGCAGCG	3360
GACCTTACCG	GCCTGAGAGAT	TCTGAGATA	TCCATCACAC	TGGCGGGCGC	TCGAGCACC	3420
CCACCAACAC	CACTGAGATC	CGGCTGTAA	CAAAGCCGA	AAGGAAGCTG	ATTTGGCTG	3480
TGCCACCGCT	GAGCAATAAC	TAGCATAAAC	CCTTGGGGCC	TCTAACGGG	TCTTGAGGGG	3540
TTTTTGCTG	AAAGGAGGA	CTATATCCGG	AT			3572

## (2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

Val	Gln	Phe	Gln	Ser	Gly	Gly	Asp	Asn	Ser	Pro	Ala	Val	Tyr	Xaa	Xaa
1				5					10				15		
Asp	Gly	Xaa	Arg												20

## (2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

Thr	Thr	Val	Pro	Xaa	Val	Thr	Glu	Ala	Arg
1					5				10

## (2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

Thr	Thr	Pro	Ser	Xaa	Val	Ala	Phe	Ala	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1000848473 022506

1 5 10

## (2) INFORMATION FOR SEQ ID NO:346:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Asp Ala Gly Lys Xaa Ala Gly Xaa Asp Val Xaa Arg  
 1 5 10

## (2) INFORMATION FOR SEQ ID NO:347:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

Thr Xaa Glu Glu Xaa Gln Glu Ser Phe Asn Ser Ala Ala Pro Gly Asn  
 1 5 10 15  
 Xaa Lys

## (2) INFORMATION FOR SEQ ID NO:348:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Other

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

CTAGTTAGTA CTCAGTCGCA GACCGTG

27

## (2) INFORMATION FOR SEQ ID NO:349:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

GCAGTGACGA ATTCACTTCG ACTCC

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(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

CATATGGGCC	ATCATCATCA	TCATCACGTG	ATCGACATCA	TCGGGACCCAG	CCCCACATCC	60
TGGGAAACAGG	CGGGGGCGGA	GGCGGTCCAG	CGGGCGCGGG	ATAGCGCTGA	TGACATCCG	120
GTCGCTCGGG	TCAATTGAGCA	GGACATGGCC	GTGGACAGCG	CGGGCAAGAT	CACCTTACCGC	180
ATCAAGCTCG	AAGTGTGCG	CAAGATGAGG	CGGGCGCAAC	CGAGGGGGCTC	GAACACCACCG	240
AGCGGTTCCG	CTGAAACGGG	CGGGGGCGGC	GGTACTGTCC	CGACTACCCC	CGCGTGTGCG	300
CCGGGTGACGT	TGGCGGAGAC	CGGTAGCACG	CTGCTTACCC	CGCTGTCAA	CCTGTGGGGT	360
CCGGCCCTTC	ACGAGAACGT	TCGGCAACCTC	ACGATCACCC	CTCAGGGCAC	CGGTCTCTG	420
GCGGGGATCG	CGGAGGGCG	CGGGGGCGAC	GTCAAATCTG	GGGGCTCCGA	CGCCCTATCTG	480
TCGGAAGGTTG	ATATGGCCG	GCACAAGGGG	CTGATGAA	TCGGCTAGC	CATCTCCGCT	540
CAGCAGGCTCA	ACTACAACT	GCCGGGAGTG	AGGGACGAC	TCAAGCTGAA	CGGAAAAGTC	600
CTGGGGGGCA	TGTGACCGGG	CACCATCAA	ACCTGGGACG	ACCCGGAGAT	CGCTGGGCTC	660
AACCCCGCGC	TGAACCTGCC	CGGCACCGCG	GTAGTTCGCC	TGCACCGCTC	CGACGGGTCC	720
GGTGTACACT	TCTTGTTCAC	TCGAGTCTTC	TCGAAAGCA	ATCCCGAGGG	CTGGGGCAAG	780
TGGCCCGGT	TCGGCACACC	CGTGGACTTC	CGGGCGGTG	CGGGTGCCTG	GGGTGAGAAC	840
GGCAACGGCG	GCATGGTAC	CGGTTGGCC	GAGACACCGG	GTCGCTGGC	CTATATCGC	900
ATCAGCTTC	TCGACCAGGC	CAGTCACCGG	AGGACTCGCC	AGGCCCAACT	AGGCAATATGC	960
TCTGCAATT	TCTTGTTCG	CGACGGCAAA	AGCATTCAGG	CGGGCGGGC	TGGCTTCGCA	1020
TCGAAACACC	CGCGAACCA	GGCATTTCG	ATGATCGACG	GGCCCGCCCC	GGACGGCTAC	1080
CCGATCATCA	ACTACAGTC	CGCCATCTC	AACCAACCGG	AAAGGACGCG	CGCCACCGCG	1140
CAGACATTCTC	AGGCATTTC	GCACGGGCG	ATCACCGACG	GCACAAAGGC	CTCGTTCTCG	1200
GACCAAGGTT	ATTTCCAGCC	GCTGCCGCC	CGGGTGGTGA	AGTTGTCGA	CGCGTTGATC	1260
GCAGGAGATT	CCAGCTGGCA	GATGAGAAC	GATGCCCTA	CCCTCCGGCA	GGAGGGCAGG	1320
AATTCTGAGC	GGATCTCCG	CGACCTGAAA	ACCCAGATCG	ACCAAGTGG	GTGACGGCA	1380
GGTTCTGTG	AGGGCCAGTG	CGCGCGCGCG	CGGGGACGG	CGGCCAGGC	CGCGGTGGTG	1440
CGCTTCCAAAG	AGGAGGCCAA	TAAGCAGAAG	CAGGAACATCG	ACGAGATCTC	GACGAATATT	1500
CGTCAGGGCG	GGGTCAATA	CTCGAGGGCC	GACGAGGAGC	AGCAGCAGGC	GCTGTCTCG	1560
CAAATGGGCT	TTGTGCCAC	AACGGCCGCC	TCGCCGCCGT	CGACCGCTGC	AGCGCCACCC	1620
GCACCCGGCGA	CCACTGTGTC	CCCCCCCA	CGGGCGCGG	CCAAACACGCC	GAATGCCCA	1680
CGGGGGGATC	CCAACGGCACG	ACCTCTGGCC	CGCCACGGCA	ACGCACCGCC	GCCACCTGTC	1740
ATTGCCCAA	ACGCACCCCA	ACCTGTCCG	ATCGACAAAC	CGGTTGGAGG	ATTCACTTC	1800
GGGCTGCTCTG	CTGGCTGGGT	GGAGTCTGAC	GGCCGCCACT	CTGACTACGG	TTCACTGACTC	1860
CTCAGCAA	ACCAAGGGGA	CCCGGCAATT	CCCCGACAGC	CGCGGCCGGT	GGCCAAATGAC	1920
ACCCGATACG	TGCTCGGGCG	GCTAGACCAA	AAAGCTTACG	CCAGCGCCGA	AGCCACCGAC	1980
TCCAAGGGCG	CGGGCTGGGT	GGGCTGAC	ATGGGTGAGT	TCTATATGCC	CTACCCGGGC	2040
ACCCGATCA	ACCAAGAAAC	CGTCTCGCTC	GACCGCAACG	GGGTGTCCTG	AAAGCGCTCG	2100
TATTAGAAG	TCAAGTTCAG	CGATCCGAGT	AAGCCGAACG	GCCAGATCTG	GACGGCGTGA	2160

ATCGGCTCG	CCGCGGCGAA	CGCACCGGAC	GCCGGGCC	CTCAGCGCTG	TTTTGTGGTA	2220
TGGCTCGGGA	CCGCCAACAA	CCGGTGGAC	AAGGGCGGG	CCAAGCGCT	GGCCGAATCG	2280
ATCGGGCTT	TGGTCGCC	GGCGCCGGG	CCGGCACCGG	CTCCCTGCAGA	GCCCCGCTCG	2340
GCGCCCGCGC	CGGCCGGGA	AGTCGCTCCT	ACCCCGACCGA	CACCGACACC	GCAGCGGACC	2400
TTACCGGCC	TA					2412

## (2) INFORMATION FOR SEQ ID NO:351:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

Met	Gly	His	His	His	His	His	Val	Ile	Asp	Ile	Ile	Gly	Thr	Ser	
1							5			10			15		
Pro	Thr	Ser	Trp	Glu	Gln	Ala	Ala	Ala	Glu	Ala	Val	Gln	Arg	Ala	Arg
							20			25			30		
Asp	Ser	Val	Asp	Asp	Ile	Arg	Val	Ala	Arg	Val	Ile	Glu	Gln	Asp	Met
							35			40			45		
Ala	Val	Asp	Ser	Ala	Gly	Lys	Ile	Thr	Tyr	Arg	Ile	Lys	Leu	Glu	Val
							50			55			60		
Ser	Phe	Lys	Met	Arg	Pro	Ala	Gln	Pro	Arg	Gly	Ser	Lys	Pro	Pro	Ser
							65			70			75		80
Gly	Ser	Pro	Glu	Thr	Gly	Ala	Gly	Ala	Gly	Thr	Val	Ala	Thr	Thr	Pro
							85			90			95		
Ala	Ser	Ser	Pro	Val	Thr	Leu	Ala	Glu	Thr	Gly	Ser	Thr	Leu	Leu	Tyr
							100			105			110		
Pro	Leu	Phe	Asn	Leu	Trp	Gly	Pro	Ala	Phe	His	Glu	Arg	Tyr	Pro	Asn
							115			120			125		
Val	Thr	Ile	Thr	Ala	Gln	Gly	Thr	Gly	Ser	Gly	Ala	Gly	Ile	Ala	Gln
							130			135			140		
Ala	Ala	Ala	Gly	Thr	Val	Asn	Ile	Gly	Ala	Ser	Asp	Ala	Tyr	Leu	Ser
							145			150			155		160
Glu	Gly	Asp	Met	Ala	Ala	His	Lys	Gly	Leu	Met	Asn	Ile	Ala	Leu	Ala
							165			170			175		
Ile	Ser	Ala	Gln	Gln	Val	Asn	Tyr	Asn	Leu	Pro	Gly	Val	Ser	Glu	His
							180			185			190		
Leu	Lys	Leu	Asn	Gly	Lys	Val	Leu	Ala	Ala	Met	Tyr	Gln	Gly	Thr	Ile
							195			200			205		
Lys	Thr	Trp	Asp	Asp	Pro	Gln	Ile	Ala	Ala	Leu	Asn	Pro	Gly	Val	Asn
							210			215			220		
Leu	Pro	Gly	Thr	Ala	Val	Val	Pro	Leu	His	Arg	Ser	Asp	Gly	Ser	Gly
							225			230			235		240
Asp	Thr	Phe	Leu	Phe	Thr	Gln	Tyr	Leu	Ser	Lys	Gln	Asp	Pro	Glu	Gly
							245			250			255		
Trp	Gly	Lys	Ser	Pro	Gly	Phe	Gly	Thr	Thr	Val	Asp	Phe	Pro	Ala	Val
							260			265			270		
Pro	Gly	Ala	Leu	Gly	Glu	Asn	Gly	Gly	Met	Val	Thr	Gly	Cys		
							275			280			285		
Ala	Glu	Thr	Pro	Gly	Cys	Val	Ala	Tyr	Ile	Gly	Ile	Ser	Phe	Leu	Asp

1003434200205200

290	295	300
Gln Ala Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser		
305	310	315
Gly Asn Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala		320
325	330	335
Gly Phe Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp		
340	345	350
Gly Pro Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile		
355	360	365
Val Asn Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala		
370	375	380
Phe Leu His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp		
385	390	395
Gln Val His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp		400
405	410	415
Ala Leu Ile Ala Thr Ile Ser Ser Ala Glu Met Lys Thr Asp Ala Ala		
420	425	430
Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile Ser Gly Asp Leu		
435	440	445
Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln Gly		
450	455	460
Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala Ala Val Val Arg		
465	470	475
Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile Ser		480
485	490	495
Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu Glu		
500	505	510
Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe Val Pro Thr Thr Ala		
515	520	525
Ala Ser Pro Pro Ser Thr Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro		
530	535	540
Val Ala Pro Pro Pro Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro		
545	550	555
Gly Asp Pro Asn Ala Ala Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro		560
565	570	575
Pro Pro Val Ile Ala Pro Asn Ala Pro Gln Pro Val Arg Ile Asp Asn		
580	585	590
Pro Val Gly Gly Phe Ser Phe Ala Leu Pro Ala Gly Trp Val Glu Ser		
595	600	605
Asp Ala Ala His Phe Asp Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr		
610	615	620
Gly Asp Pro Pro Phe Pro Gly Gln Pro Pro Pro Val Ala Asn Asp Thr		
625	630	635
Arg Ile Val Leu Gly Arg Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu		640
645	650	655
Ala Thr Asp Ser Lys Ala Ala Ala Arg Leu Gly Ser Asp Met Gly Glu		
660	665	670
Phe Tyr Met Pro Tyr Pro Gly Thr Arg Ile Asn Gln Glu Thr Val Ser		
675	680	685
Leu Asp Ala Asn Gly Val Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys		
690	695	700
Phe Ser Asp Pro Ser Lys Pro Asn Gly Gln Ile Trp Thr Gly Val Ile		
705	710	715
Gly Ser Pro Ala Ala Asn Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp		720
725	730	735

Phe Val Val Trp Leu Gly Thr Ala Asn Asn Pro Val Asp Lys Gly Ala  
 740 745 750  
 Ala Lys Ala Leu Ala Glu Ser Ile Arg Pro Leu Val Ala Pro Pro Pro  
 755 760 765  
 Ala Pro Ala Pro Ala Pro Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala  
 770 775 780  
 Gly Glu Val Ala Pro Thr Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu  
 785 790 795 800  
 Pro Ala

## (2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 34 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

GGATCCAAAC CACCGAGCGG TTTCGCTGAA AC GG

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## (2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

CGCTGCGAAT TCACCTCCGG AGGAAATCGT CGCGATC

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## (2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1962 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

CATATGGGCC ATCATCATCA TCATCACCGA TCCAAACAC CGAGCGGTTG GCCTGAAAGC  
 GGGCCGGCG CGCGTACTGT CGCGACTAAC CCCCGCTGCTG CGCGGGTGAC GTTGGCGGAG  
 ACCGGTAGCA CGCTGCTCTA CCCGGCTGTT AACCTGTTGG GTCCGGCCTT TCACGGAGAGG  
 TATCCGAAACG TCACGATCAC CGCTCAGGGC ACCGGTTCTG GTGCCGGGAT CGCGCAGGCC

60

120

180

240

GGCGCCGGGA	CGGTCAACAT	TGGGCCCTCC	GACGCCATAC	TGTCGGAAGG	TGATATGGCC	300
GGCACAAAGG	GGCTGATGAA	CATCGCGTA	GCCATCTCGG	CTCAGCAGGT	CAACTAACAC	360
CTGCCCGAGG	TGAGCGAGCA	CCTCAAGCTG	AACGGAAAAG	TCCCTGGCGGC	CATGTACCAAG	420
GGCACCATCA	AAACCTGGGA	CGACCCCGAG	ATCGCTGGCC	TCAACCCCGG	CGTGAAACCTG	480
CCGGCACCG	CGGTACTTCC	GCTGACCGC	TCCGACGGGT	CCGGTGACAC	CTTCTTGTTTC	540
ACCCAGTAC	TGTCCAAGCA	AGATCCCGAG	GGCTGGGCA	AGTCGCGGG	CTTCGGCACC	600
ACCGTCAACT	TCCCGGGCGGT	GCCGGGTGG	CTGGGTGAGA	ACGGCAACGG	CGGCATGTTG	660
ACCGGTTCGG	CGGAGACACC	GGGCTCGCTG	GCCTATATCG	GCATCAGCTT	CCTCGACCAAG	720
GCCAGTCAAC	GGGGACTCGG	CGAGGCCAA	CTAGGCAATA	GCTCTGGCA	TTCTTGTG	780
CCCGACCGC	AAAGGCTACCA	GGCCCGGGG	GCTGGCTTCG	CATCGAAAC	CCCGCGACAC	840
CAGGGATTT	CGATGATCGA	CGGGCCGCC	CGGAGCGGT	ACCGGATCAT	CAACTACGG	900
TACGGCATCG	TCAACAAACCG	GCAAAAGGAC	GCGGCCACCG	CGCAGACCTT	GCAGGATT	960
CTGCACTGGG	CGATCACCGA	CGGACACAG	GCCTCGTTC	TCGACCGAGT	TCATTTCCAG	1020
CCGCTGCCGC	CCCGCTGGTG	GAAGTTGTC	TCAGCGTTCA	TCGGCACGAT	TTCTCCGG	1080
GGTGGCAGTG	GGGGAGGCTC	AGGTGGAGGT	TCTGGGGG	CGCTGCCAC	AACGGCGCC	1140
TGCGCCGGCT	CGACCCGAC	AGCGCCACCC	GCACCCGGGA	CACCTGTTGC	CCCCCCACCA	1200
CCGGCCGCCG	CCAACACCGC	GAATGCCAG	CGGGCGATC	CCAAACGCGAC	ACCTCCGGC	1260
GCCGACCCGA	ACGCACCGC	GCCACCTGTG	ATTGCCCAAA	ACGACCCCCA	ACCTGTCCGG	1320
ATCGAACACC	CGGTTGGAGG	ATTCACTTC	CGCGCTGGCTG	CTGGCTGGGT	GGAGTCTGAC	1380
GCCGCCCACT	TGCACTACCG	TTCACTAC	CTCAGCAAAA	CCACCGGGGA	CCCCGATTT	1440
CCGGACACGC	CCGGCCGGCT	GCCCAATGAC	ACCCGTATCG	TGCTGGGG	GCTAGACCAA	1500
AAGCTTACO	CCAGCGCCGA	AGCCACCGAC	TCCAAGGGCG	CGGCCCGGTT	GGGCTCGGAC	1560
ATGGGTGAGT	TCTATATGCC	CTACCGGGC	ACCCGGATCA	ACAGGAAAC	CGTCTCGTC	1620
GACGCCAACO	GGGTGCTCG	AAAGCGCTG	TATTACGAAAG	TCAAGTTACG	CGATCGGAGT	1680
AAGCGAACCC	CGGAGACTCTG	GACGGCGCTA	ATCGGCTCG	CGCGGGCGAA	CGCACCGGAC	1740
GCGGGCCCG	CTCAGCGCTG	GTTCGTTGGA	TGGCTGGGA	CGGCCAACAA	CCCGGTGGAC	1800
AAGGGCGCGG	CCAAGGGCGT	GCGCGAACATG	ATCCGGCTT	TGGTCGCCCC	GCCGCCGGCG	1860
CCGGCACCGG	CTCTCGAGA	GCCCGCTCGG	GGCGCGGGCG	CGGCCGGGGA	AGTCGCTCCT	1920
ACCCGACG	CACCGACACC	GCAGCGGAC	TTACCGGCC	GA		1962

## (2) INFORMATION FOR SEQ ID NO:355:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 652 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

Met	Gly	His	His	His	His	His	Gly	Ser	Lys	Pro	Pro	Ser	Gly	Ser	
1							5		10			15			
Pro	Glu	Thr	Gly	Ala	Gly	Ala	Gly	Thr	Val	Ala	Thr	Thr	Pro	Ala	Ser
															30
Ser	Pro	Val	Thr	Leu	Ala	Glu	Thr	Gly	Ser	Thr	Leu	Leu	Tyr	Pro	Leu
															35
Phe	Asn	Leu	Trp	Gly	Pro	Ala	Phe	His	Glu	Arg	Tyr	Pro	Asn	Val	Thr
															50
Ile	Thr	Ala	Gln	Gly	Thr	Gly	Ser	Gly	Ala	Gly	Ile	Ala	Gln	Ala	65
															70
Ala	Gly	Thr	Val	Asn	Ile	Gly	Ala	Ser	Asp	Ala	Tyr	Leu	Ser	Glu	Gly
															85
Asp	Met	Ala	Ala	His	Lys	Gly	Leu	Met	Asn	Ile	Ala	Leu	Ala	Ile	Ser
															90
															95

100	105	110	
Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys			
115	120	125	
Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr			
130	135	140	
Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro			
145	150	155	160
Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr			
165	170	175	
Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly			
180	185	190	
Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly			
195	200	205	
Ala Leu Gly Glu Asn Gly Asn Gly Met Val Thr Gly Cys Ala Glu			
210	215	220	
Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala			
225	230	235	240
Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn			
245	250	255	
Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Gly Phe			
260	265	270	
Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro			
275	280	285	
Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn			
290	295	300	
Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu			
305	310	315	320
His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val			
325	330	335	
His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu			
340	345	350	
Ile Ala Thr Ile Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly			
355	360	365	
Gly Ser Gly Gly Ser Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr			
370	375	380	
Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro			
385	390	395	400
Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala			
405	410	415	
Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Val Ile Ala Pro			
420	425	430	
Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser			
435	440	445	
Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp			
450	455	460	
Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro			
465	470	475	480
Gly Gln Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg			
485	490	495	
Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala			
500	505	510	
Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro			
515	520	525	
Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val			
530	535	540	

Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys  
545 550 555 560  
Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn  
565 570 575  
Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly  
580 585 590  
Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu  
595 600 605  
Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro  
610 615 620  
Ala Glu Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr  
625 630 635 640  
Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala  
645 650